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(54) Title: METHOD AND REAGENT FOR PREVENTION, INHIBITION OF PROGRESSION AND REGRESSION OF VASCULAR DISEASES			
(57) Abstract			
A nucleic acid molecule which blocks synthesis and/or expression of mRNAs associated with initial development, progression or regression of vascular disease. In particular are provided ribozyme sequences which cleave human or rabbit cholesterol ester transfer protein (CETP) mRNAs.			

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DESCRIPTIONMethod and Reagent for Prevention, Inhibition of Progression and Regression of Vascular DiseasesBackground Of The Invention

This invention relates to the methods for the prevention, inhibition of progression and regression of vascular diseases, in particular, inhibition of cholesterol ester transfer protein (CETP) inhibition.

5 The following is a discussion of relevant art, none of which is admitted to be prior art to the present invention.

Vascular diseases, which includes etiologies such as 10 peripheral vascular disease, coronary heart disease (CHD), stroke and restenosis, remain the leading cause of death and disability in the United States and throughout the world. In 1990 alone, approximately 500,000 people died in the United States from CHD. Although, diet and life 15 style can accelerate the rate of onset of vascular diseases, genetic predisposition leading to "dyslipidemia" is a major and significant factor attributing to vascular related deaths and disabilities (Anderson et al., 1987 JAMA 257, 2176). By "dyslipidemia" is meant abnormal 20 levels of lipoproteins in plasma.

A variety of risk factors have been identified that are associated with increased risk of vascular disease (Barr et al., 1951 Am. J. Med. 11, 480; Kannel et al., 1971 Ann. Intern. Med. 74, 1; Miller et al., 1975 Lancet 25, 1, 16; Levy et al., 1984 Circulation 69, 325.; Lipid Research Clinics Program, 1984 JAMA 251, 351; Lipid Research Clinics Program, 1984 JAMA 251, 365; Anderson et al., 1987 JAMA 257, 2176; Blankenhorn et al., 1987 J. Am. Med. Assoc. 257, 3233.; Frick et al., 1987 N. Engl. J. Med. 317, 1237; Expert Panel, 1988 Arch. Intern. Med. 148, 36.; Grundy et al., 1989 Arch. Intern. Med. 149, 505.; La Rosa, 1990 Am. J. Cardiol. 65, 7F-10F). Among these are

the dyslipidemias of high levels of low density lipoproteins (LDL) and low levels of high density lipoproteins (HDL), singly or in combination. Often the ratio of HDL cholesterol to that of LDL cholesterol is used to assess 5 risk of vascular disease. Thus, a high ratio of HDL/LDL cholesterol is desirable, and intervention to increase the ratio by lowering LDL and elevating HDL, singly or in combination is desirable.

Familial hypercholesterolemia (FH), a genetic disorder caused by defective or deficient LDL receptors presents as a marked elevation in LDL and risk in vascular disease (Goldstein et al., 1989 "Familial hypercholesterolemia" In: The Metabolic Basis of Inherited Diseases, 6th Ed., Schriver, C.R., Beaudet, A.L., Sly, W.S., and Valle, 15 D. editors, 1215). Homozygous FH is a relatively rare disorder (1 in 1,000,000). Homozygous FH patients have extremely high levels of LDL with very short life expectancies. Therapy for these individuals include liver transplantation and LDL plasmaphoresis. Heterozygous FH 20 is relatively common disorder (1 in 500). Heterozygous FH patients present with LDL levels approximately twice normal and are at risk for developing premature atherosclerosis followed by the common sequelae associated with vascular diseases, including myocardial infarction and 25 stroke. Conventional therapy for heterozygous FH patients generally includes HMG CoA reductase inhibitors alone or in combination with bile acid sequestrants. Human prospective trials have demonstrated reduction in CHD related endpoints in hypercholesterolemic subjects treated 30 with HMGCoA reductase inhibitors, bile acid sequestrants, Nicotinic acid, and gemfibrozil (La Rosa, 1990 Am. J. Cardiol. 65, 7F; Pedersen et al., 1994 Lancet 344, 1383).

Other conditions, such as apoE 3/4 and apoE4/4 genotype are also associated with increased LDL elevation and 35 risk of CHD. However the direct causal relation between apoE4 polymorphism, elevated LDL and increased risk is unknown (Davignon et al., 1988 Arteriosclerosis 8, 1;

Dallongeville et al., 1992 J. Lipid Res. 33, 447; Walden et al., 1994 Ann. Intern. Med. 120, 1026).

Low levels of HDL or hypoalphalipoproteinemia is a relatively common condition. The genetic basis for hypoalphalipoproteinemia is poorly understood, but likely results from multiple factors related to genetic predisposition and life style. Numerous prospective and retrospective studies have shown that HDL is inversely and strongly correlated with vascular disease. Therefore treatment to elevate HDL levels is warranted (Grundy et al., 1989 Arch. Intern. Med. 149, 505). It is also well recognized, that plasma triglyceride elevation is generally associated with low HDL levels, and insulin resistance (Reaven, 1988 Diabetes 37, 1595). Conventional therapies for elevated triglycerides and low HDL generally include treatment with fibrates. Gemfibrozil, a compound of this class, effectively lowers plasma triglycerides, and moderately elevates HDL (Frick, 1987 N. Engl. J. Med. 317, 1237). In a large human prospective trial, gemfibrozil has been shown to cause a significant reduction in vascular endpoints (Frick, 1987 supra).

The process termed reverse cholesterol transport (RCT; Bailey, 1965 Exp. Cell. Res. 37, 175; Glomset, 1968 J. Lipid Res. 9, 155) is a mechanism resulting in a net efflux of cholesterol present in peripheral tissues for disposal in bile. This multistep "hypothesized" pathway invokes removal of cholestryol from peripheral tissues to HDL. Lecithin: cholesterol acyltransferase (LCAT), a circulating plasma enzyme, primarily mediates the esterification of HDL cholesterol to cholestryol esters. CETP, also present in plasma, mediates HDL cholestryol ester net transfer to apolipoprotein B (apoB)-containing lipoproteins including very low density lipoproteins (VLDL), intermediate density lipoproteins or remnants (IDL) and LDL. CETP-mediated cholestryol ester enrichment of the LDL precursors, VLDL and IDL, ultimately contributes to the cholesterol content of LDL. Hepatic receptor-mediated

LDL uptake, and a net flux of these delivered cholesteryl esters to the bile acid pool completes RCT. However, species that lack CETP (Oschry et al., 1982 J. Lipid Res. 23, 1099) or humans deficient in CETP (Koizumi et al., 5 1985 Atherosclerosis 58, 175) are unable to effectively transfer cholesteryl esters formed in HDL to the LDL precursor pool. Although the break in this link of the RCT pathway might predictably result in a marked deficiency in peripheral tissue cholesterol egress, 10 surprisingly, this is not the case. In CETP deficient species, the HDL cholesteryl ester pool accumulates at the expense of the LDL pool. The HDL particles become enlarged and apoA-I, apoA-IV, and apoE-enriched (Brown et al., 1989 Nature 342, 448-451; Yamashita et al., 1990 J. 15 Clin. Invest. 86, 688; Bisgaier et al., 1991 J. Lipid Res. 32, 21). Particles containing apoE can effectively be delivered to the liver as whole particles by facilitated mechanisms, including those utilizing the LDL receptor and the LDL receptor related protein (LRP) (Goldstein et al., 20 1985 Ann. Rev. Cell Biol. 1, 1; Mahley, 1988 Science 240, 622.; Beisiegel et al., 1989 Nature 341, 162; Bisgaier et al., 1989 J. Biol. Chem. 264, 862.). Thus, alternative mechanisms exist that facilitate tissue cholesterol egress and delivery of non-LDL cholesterol to liver in the 25 absence of CETP.

Thus, CETP inhibition may inhibit or eliminate the RCT pathway thereby preventing the reduction in size and density of HDL, prolonging HDL half-life, and resulting in increased HDL levels. Additionally, the lack of transport 30 of cholesteryl esters from HDL to apoB-containing lipoproteins may reduce LDL concentrations. Both these effects would result in an elevation of the HDL to LDL ratio. As high HDL/LDL ratios and HDL levels have been associated with anti-atherogenicity, diminishing CETP 35 activity may prevent or inhibit progression and regression of vascular disease.

CETP is a 74 kDa glycoprotein that facilitates neutral lipid (cholesteryl esters and triglycerides) transfer between plasma lipoproteins (Zilversmit et al., 1975 Biochim. Biophys. Acta 409, 393; Ha et al., 1982 5 Comp. Biochem. Physiol. 71B, 265; Drayna et al., 1987 Nature 327, 632; Hesler et al., 1987 J. Biol. Chem. 262, 2275; Swenson et al., 1987 J. Biol. Chem. 262, 16271; Hesler et al., 1988 J. Biol. Chem. 263, 5020; Nagashima et al., 1988 J. Lipid Res. 29, 1643; Pape et al., 1991 10 Arterioscler. Thromb. 11, 1759). In non-human primates and rabbits, hepatic non-parenchymal cells are likely the major synthetic source of CETP (Pape et al., 1991 Arterioscler. Thromb. 11, 1759; Pape et al., 1991 J. Biol. Chem. 266, 12829; Rea et al., 1993 J. Lipid Res. 34, 15 1901), in that these cells have the highest cellular content of CETP mRNA relative to total RNA. Abundant amounts of CETP mRNA has also been shown in hepatic parenchymal cells, adipose, and spleen and to a lesser extent in the intestine and heart.

20 The level of CETP activity between species is highly variable (Ha et al., 1982 Comp. Biochem. Physiol. 71B, 265; Bisgaier et al., 1993 J. Lipid Res. 34, 1625). In general, species with high CETP activity (e.g., humans and rabbits) are susceptible to dietary induced atherosclerosis, while species with little or no CETP activity (e.g., mice, rats and dogs) are resistant (Koizumi et al., 1985 25 Atherosclerosis 58, 175; Inazu et al., 1990 N. Engl. J. Med. 323, 1234; Agellon et al., 1991 J. Biol. Chem. 260, 10796; Bisgaier et al., 1991 J. Lipid Res. 32, 21; Marotti 30 et al., 1992 Arterioscler. Thrombosis 12, 736). Likewise, those species with little or no CETP activity have anti-atherosclerotic lipoprotein profiles: plasma HDL levels are elevated and LDL are reduced (Ha et al., 1982 Comp. Biochem. Physiol. 71B, 265). Infusions of inhibitory CETP 35 monoclonal or polyclonal antibodies into rabbits or infusion of CETP into rats will invert the lipoprotein profiles (Ha et al., 1985 Biochim. Biophys. Acta 833,

203; Abbey et al., 1989 Biochim. Biophys. Acta 1003, 20;
Groener et al., 1989 Biochim. Biophys. Acta 1002, 93;
Whitlock et al., 1989 J. Clin. Invest. 84, 129.). Unlike
control mice of similar genetic background, CETP trans-
5 genic mice develop atherosclerotic lipoproteins and
atherosclerosis (Marotti et al., 1992 Arterioscler.
Thromb. 12, 736).

Recent studies of a Japanese family have shown that
a deficiency in plasma CETP associated with marked eleva-
10 tion of HDL, its associated apolipoproteins (apoA-I, apoE,
apoA-IV) and a rarity of coronary artery disease (Koizumi
et al., 1985 Atherosclerosis 58, 175; Brown et al., 1989
Nature 342, 448; Inazu et al., 1990 N. Engl. J. Med. 323,
1234; Bisgaier et al., 1991 J. Lipid Res. 32, 21.; Ikewaki
15 et al., 1991 Arterioscler. Thromb. 11, 1400a; Koizumi et
al., 1991 Atherosclerosis 90, 189). These individuals
were identified through routine cholesterol screening and
have no other hyperlipidemia related disease. The defect
has been identified as a G to A substitution in the
20 fourteenth intron of CETP pre-messenger ribonucleic acid
(RNA) (Brown et al., 1989 Nature 342, 448). This splice
donor defect is also the cause of the deficiency in
additional Japanese families (Inazu et al., 1990 N. Engl.
J. Med. 323, 1234; Koizumi et al., 1991 Atherosclerosis
25 90, 189; Hirano et al., 1993 Atherosclerosis 100, 85). In
a more recent study, the deficiency (both homozygous and
heterozygous) has been shown to be associated with a large
proportion of Japanese with hyperalphalipoproteinemia
(Inazu et al., 1992 Horm. Metab. Res. 24, 284; Hirano et
30 al., 1993 Atherosclerosis 100, 85). A missense mutation
at nucleotide 1506 (G for A) also has been identified in
exon 15 of the CETP gene, resulting in a substitution of a
glycine for aspartic acid at amino acid 442 (Takahashi et
al., 1993 J. Clin. Invest. 92, 2060). The two subjects
35 heterozygous for the missense mutation had three times the
normal HDL levels. Overall these studies suggest that
even partial reduction in CETP levels, as found in

heterozygous individuals, is associated with elevated HDL. This apparently benign condition (CETP deficiency) has been coined the "longevity syndrome" (Koizumi et al., 1985 Atherosclerosis 58, 175).

5 Although CETP facilitates an equimolar exchange of neutral lipids, net transfer of cholestryl ester to LDL occurs due to (1) concentration and core lipid composition of exchange partners and (2) residence time of lipoproteins (Nichols et al., 1965 J. Lipid. Res. 206; Pattaik
10 et al., 1978 Biochim. Biophys. Acta 530, 428; Barter et al., 1979 Metabolism 28, 230). Under basal conditions (i.e., overnight fast), CETP facilitates transfer below maximal velocity, while postprandially CETP appears to facilitate transfer at or near maximal velocity (Tall et
15 al., 1986 J. Clin. Invest. 77, 1163; Mann et al., 1991 J. Clin. Invest. 88, 2059; Bisgaier et al., 1993 J. Lipid Res. 34, 1625). It is also likely, but has not been systematically shown, that individuals with elevated triglycerides would have elevated CETP activity (but not necessarily increased CETP mass). In general, these subjects have reduced levels of HDL and elevated LDL. These consequences, in part may be the result of events facilitated by CETP.

20 The complete amino acid sequence of human, rabbit, cynomolgus monkey and hamster CETP are known (Drayna et al., 1987 Nature 327, 632; Nagashima et al., 1988 J. Lipid Res. 29, 1643; Jiang et al., 1991 J. Biol. Chem. 266, 4631; Pape et al., 1991 Arterioscler. Thromb. 11, 1759). Human plasma levels are approximately 1-2 µg/ml, while rabbit levels are approximately 4 µg/ml. Cholesterol feeding in rabbits elevates tissue CETP mRNA, plasma CETP, and maximal plasma activity approximately 4 fold (Quinet et al., 1990 J. Clin. Invest. 85, 357; McPherson et al., 1991 Arterioscler. Thromb. 11, 797). The protein is stable to heat, limited proteolysis, but not oxidation. CETP has been mapped with neutral and inhibitory monoclonal antibodies and by site-directed mutagenesis

(Hesler et al., 1987 J. Biol. Chem. 262, 2275; Hesler et al., 1988 J. Biol. Chem. 263, 5020; Wang et al., 1991 Biochemistry 30, 3484). Stable transfection of the human gene in CHO cells has been accomplished (Wang et al., 1991 5 Biochemistry 30, 3484; Wang et al., 1992 J. Biol. Chem. 267, 17487). However, the protein has not been crystalized nor have the lipid binding domains been identified. Furthermore, the mechanisms by which CETP facilitates transfer are poorly understood.

10 Direct pharmacological inhibition of the existing protein in plasma or targeting CETP gene expression might lead to reduced plasma activity and result in a beneficial lipoprotein profile (*i.e.*, HDL elevation and LDL diminution) and a reduced risk of coronary heart disease. 15 However a synthetic compound approach for the direct inhibition of the plasma CETP has not yet been promising (Bisgaier et al., 1994 Lipids 29).

The gene encoding CETP is composed of 16 exons of various sizes (32-250 bp) and spans approximately 25 kb on 20 the long arm (q12-21) of chromosome 16 (Lusis et al., 1987 Genomics 1, 232; Agellon et al., 1990 Biochemistry 29, 1372). Cloning and sequencing of the human CETP cDNA has been reported and shown to contain an open reading frame and 3' untranslated region of 1656 nucleotides in length 25 (Drayna et al., 1987 Nature 327, 632). Analysis of amino-acid and nucleic acid sequence has indicated a protein that is unique among eukaryotic species. A pentanucleotide amino acid stretch in the precursor protein signal peptide of CETP is conserved among the lipid metabolism 30 associated proteins, for example apoA-IV, apoA-I, and lipoprotein lipase (Agellon et al., 1990 Biochemistry 29, 1372). This conservation occurs at both the nucleotide and the amino-acid level. This small but highly conserved region is found only in the precursor protein species and 35 is removed before secretion of the mature protein into the blood stream. Other less conserved homologies have been noted with two lipopolysaccharide binding proteins, bac-

terial permeability increasing protein found in leukocyte granules and plasma lipopolysaccharide binding protein (Tall, 1993 J. Lipid Res. 34, 1255).

A single predominant splicing variant of the CETP message has been identified and characterized. This variant CETP mRNA lacks exon 9 and accounts for between 14-46% of total CETP mRNA with the highest percentage of this variant seen in the spleen. While the function of this abundant splice variant is not clearly understood, when coordinately expressed with full-length CETP in Chinese Hamster Ovary (CHO) cells, it was shown not to be secreted and capable of inhibiting secretion of the full length CETP protein (Quinet et al., 1993 J. Biol. Chem. 268, 16891).

A consequence of inhibiting CETP, besides that of favorably increasing the HDL/LDL cholesterol ratio, is a change in the distribution and level of apoE. In species lacking CETP (e.g., rats), during monoclonal antibody induced inhibition of CETP in hamsters, and in human CETP deficiency, plasma apoE levels are elevated (Yamashita et al., 1990 J. Clin. Invest. 86, 688; Eto et al., 1990 Artery 17, 202; Hirano et al., 1993 Atherosclerosis 100, 85; Takahashi et al., 1993 J. Clin. Invest. 92, 2060; Bisgaier et al., 1991 J. Lipid Res. 32, 21; Evans et al., 1994 J. Lipid Res. 35, 1634). Furthermore, HDL apoE-enrichment was observed (Evans et al., 1994 J. Lipid Res. 35, 1634). Recent in vitro studies have revealed mechanisms by which apoE-enriched HDL are protective (Yamada et al., 1992 J. Clin. Invest. 706; Saxena et al., 1993 J. Biol. Chem. 268, 14812). Additional studies have also demonstrated that apoE deficiency causes profound and accelerated rates of atherosclerosis in mice, a species not normally susceptible to atherosclerosis (Plump et al., 1992 Cell 71, 343; Zhang et al., 1992 Science 258, 468). Thus an expected and desirable consequence of CETP inhibition includes elevation of apoE-rich HDL. In apoE deficiency, overexpression of apoA-I can also afford protec-

tion against atherosclerosis (Plump et al., 1994 Proc. Natl. Acad. Sci. USA 91, 9607), and elevation of this protein is also an expected consequence of CETP inhibition (Koizumi et al., 1985 Atherosclerosis 58, 175; Eto et al., 5 1990 Artery 17, 202; Hirano et al., 1993 Atherosclerosis 100, 85; Takahashi et al., 1993 J. Clin. Invest. 92, 2060).

There currently exists no practical therapeutic treatment for interfering with or blocking CETP activity 10 in humans. Although not practical, repetitive anti-CETP combined with anti-LDL plasmaphoresis resulted in favorable changes in LDL and HDL levels and HDL/LDL ratios in a limited number of human studies (Davidson, U.S. Patent 5,279,540). Although plasma CETP levels markedly 15 decreased with duration of plasmaphoresis treatments, neither anti-CETP plasmaphoresis alone nor control non-immune plasmaphoresis data were reported. Several potential inhibitors are being explored in various laboratories. These inhibitors include monoclonal antibodies and 20 an inhibitor protein recently found in baboon plasma tentatively identified as the N-terminal fragment of apolipoprotein C-I (Kushwaha et al., 1993 J. Lipid Res. 1993, 1285; Kushwaha et al., WO 93/11782). In the current application, a ribozyme, antisense or 2-5A-antisense or 25 triplex DNA approach is described. The advantage of these approaches is their ability to selectively target specific regions of the CETP mRNA.

Summary Of The Invention

The invention features novel nucleic acid-based 30 techniques [e.g., enzymatic RNA molecules (ribozymes), antisense nucleic acids, 2-5A antisense chimeras, triplex DNA] and methods for their use for: (1) treatment of dyslipidemias by decreasing lipoprotein risk factors, in particular, decreasing high levels of LDL or increasing 35 low levels of HDL, or a combination of both and (2) for the prevention, inhibition of progression, and regression

of vascular diseases, particularly, those diseases associated with (but not limited to) peripheral vascular disease, coronary heart disease, stroke, vascular complications of diabetes, transplant, atherectomy, and
5 angioplastic restenosis.

The uniqueness of the CETP coding region and protein afford an increased safety margin when contemplating sequence-specific therapeutics targeting of the mRNA, such as ribozymes or antisense nucleic acids or 2'-5'A antisense
10 chimeras, since there would be a reduced likelihood of non-specific activity from these therapeutics.

In a preferred embodiment, the invention features use of nucleic acid-based techniques to treat lipoprotein risk factors and/or prevent vascular diseases by inhibiting the
15 synthesis of cholestryl ester transfer protein (CETP).

Those in the art will recognize the other potential targets, for e.g., apolipoprotein B, are also suitable for treatment with nucleic acid-based techniques described in the present invention.

20 By "inhibit" is meant that the activity of CETP or level of mRNAs encoded by CETP is reduced below that observed in the absence of the nucleic acid, particularly, inhibition with ribozymes and preferably is below that level observed in the presence of an inactive RNA molecule
25 able to bind to the same site on the mRNA, but unable to cleave that RNA.

By "enzymatic nucleic acid (NA) molecule" it is meant a nucleic acid molecule which has complementarity in a substrate binding region to a specified gene target, and
30 also has an enzymatic activity which is active to specifically cleave RNA in that target. That is, the enzymatic nucleic acid molecule is able to intermolecularly cleave RNA and thereby inactivate a target RNA molecule. This complementarity functions to allow sufficient hybridization
35 of the enzymatic nucleic acid molecule to the target RNA to allow the cleavage to occur. One hundred percent

complementarity is preferred, but complementarity as low as 50-75% may also be useful in this invention.

By "equivalent" RNA to CETP is meant to include those naturally occurring RNA molecules associated with cardiovascular diseases in various animals, including human, rabbit and monkey. Such a molecule will generally contain some ribonucleotides, but the other nucleotides may be substituted at the 2'-hydroxyl position and in other locations with other moieties as discussed below.

10 By "antisense nucleic acid" is meant a non-enzymatic nucleic acid molecule that binds to another RNA (target RNA) by means of RNA-RNA or RNA-DNA or RNA-PNA (protein nucleic acid; Egholm et al., 1993 Nature 365, 566) interactions and alters the activity of the target RNA (for a 15 review see Stein and Cheng, 1993 Science 261, 1004).

By "2-5A antisense chimera" is meant, an antisense oligonucleotide containing a 5' phosphorylated 2'-5'-linked adenylate residues. These chimeras bind to target RNA in a sequence-specific manner and activate a cellular 20 2-5A-dependent ribonuclease which in turn cleaves the target RNA (Torrence et al., 1993 Proc. Natl. Acad. Sci. USA 90, 1300).

By "triplex DNA" is meant an oligonucleotide that can bind to a double-stranded DNA in a sequence-specific 25 manner to form a triple-strand helix. Triple-helix formation has been shown to inhibit transcription of the targeted gene (Duval-Valentin et al., 1992 Proc. Natl. Acad. Sci. USA 89, 504).

By "gene" is meant a nucleic acid that encodes an 30 RNA.

By "complementarity" is meant a nucleic acid that can form hydrogen bond(s) with other RNA sequence by either traditional Watson-Crick or other non-traditional types (for example, Hoogsteen type) of base-paired interactions.

35 Six basic varieties of naturally-occurring enzymatic RNAs are known presently. Each can catalyze the hydrolysis of RNA phosphodiester bonds in trans (and thus can

cleave other RNA molecules) under physiological conditions. Table I summarizes some of the characteristics of these ribozymes. In general, enzymatic nucleic acids act by first binding to a target RNA. Such binding occurs 5 through the target binding portion of a enzymatic nucleic acid which is held in close proximity to an enzymatic portion of the molecule that acts to cleave the target RNA. Thus, the enzymatic nucleic acid first recognizes and then binds a target RNA through complementary base-10 pairing, and once bound to the correct site, acts enzymatically to cut the target RNA. Strategic cleavage of such a target RNA will destroy its ability to direct synthesis of an encoded protein. After an enzymatic nucleic acid has bound and cleaved its RNA target, it is 15 released from that RNA to search for another target and can repeatedly bind and cleave new targets.

The enzymatic nature of a ribozyme is advantageous over other technologies, since the concentration of ribozyme necessary to affect a therapeutic treatment is lower. 20 This advantage reflects the ability of the ribozyme to act enzymatically. Thus, a single ribozyme molecule is able to cleave many molecules of target RNA. In addition, the ribozyme is a highly specific inhibitor, with the specificity of inhibition depending not only on the base-25 pairing mechanism of binding to the target RNA, but also on the mechanism of target RNA cleavage. Single mismatches, or base-substitutions, near the site of cleavage can completely eliminate catalytic activity of a ribozyme.

Ribozymes that cleave the specified sites in CETP 30 mRNAs represent a novel therapeutic approach to vascular disease. Applicant indicates that ribozymes are able to inhibit the activity of CETP and that the catalytic activity of the ribozymes is required for their inhibitory effect. Those of ordinary skill in the art, will find 35 that it is clear from the examples described that other ribozymes that cleave these sites in CETP mRNAs may be readily designed and are within the invention.

In preferred embodiments of this invention, the enzymatic nucleic acid molecule is formed in a hammerhead or hairpin motif, but may also be formed in the motif of a hepatitis delta virus, group I intron or RNaseP RNA (in 5 association with an RNA guide sequence) or Neurospora VS RNA. Examples of such hammerhead motifs are described by Rossi et al., 1992, Aids Research and Human Retroviruses 8, 183, of hairpin motifs by Hampel et al., EP0360257, Hampel and Tritz, 1989 Biochemistry 28, 4929, and Hampel 10 et al., 1990 Nucleic Acids Res. 18, 299, and an example of the hepatitis delta virus motif is described by Perrotta and Been, 1992 Biochemistry 31, 16; of the RNaseP motif by Guerrier-Takada et al., 1983 Cell 35, 849, Neurospora VS 15 RNA ribozyme motif is described by Collins (Saville and Collins, 1990 Cell 61, 685-696; Saville and Collins, 1991 Proc. Natl. Acad. Sci. USA 88, 8826-8830; Collins and Olive, 1993 Biochemistry 32, 2795-2799) and of the Group I intron by Cech et al., U.S. Patent 4,987,071. These 20 specific motifs are not limiting in the invention and those skilled in the art will recognize that all that is important in an enzymatic nucleic acid molecule of this invention is that it has a specific substrate binding site which is complementary to one or more of the target gene 25 RNA regions, and that it have nucleotide sequences within or surrounding that substrate binding site which impart an RNA cleaving activity to the molecule.

In a preferred embodiment the invention provides a method for producing a class of enzymatic cleaving agents which exhibit a high degree of specificity for the RNA of 30 a desired target. The enzymatic nucleic acid molecule is preferably targeted to a highly conserved sequence region of a target mRNAs encoding CETP proteins such that specific treatment of a disease or condition can be provided with either one or several enzymatic nucleic acids. Such 35 enzymatic nucleic acid molecules can be delivered exogenously to specific cells as required. Alternatively, the

ribozymes can be expressed from DNA/RNA vectors that are delivered to specific cells.

Synthesis of nucleic acids greater than 100 nucleotides in length is difficult using automated methods, and 5 the therapeutic cost of such molecules is prohibitive. In this invention, small enzymatic nucleic acid motifs (e.g., of the hammerhead or the hairpin structure) are used for exogenous delivery. The simple structure of these molecules increases the ability of the enzymatic nucleic acid 10 to invade targeted regions of the mRNA structure. However, these catalytic RNA molecules can also be expressed within cells from eukaryotic promoters (e.g., Scanlon et al., 1991, Proc. Natl. Acad. Sci. USA, 88, 10591-5; Kashani-Sabet et al., 1992 Antisense Res. Dev., 15 2, 3-15; Dropulic et al., 1992 J. Virol., 66, 1432-41; Weerasinghe et al., 1991 J. Virol., 65, 5531-4; Ojwang et al., 1992 Proc. Natl. Acad. Sci. USA 89, 10802-6; Chen et al., 1992 Nucleic Acids Res., 20, 4581-9; Sarver et al., 20 1990 Science 247, 1222-1225). Those skilled in the art realize that any ribozyme can be expressed in eukaryotic 25 cells from the appropriate DNA/RNA vector. The activity of such ribozymes can be augmented by their release from the primary transcript by a second ribozyme (Draper et al., PCT WO 93/23569, and Sullivan et al., PCT WO 94/02595, both hereby incorporated in their totality by reference herein; Ohkawa et al., 1992 Nucleic Acids Symp. Ser., 27, 15-6; Taira et al., 1991, Nucleic Acids Res., 19, 5125-30; Ventura et al., 1993 Nucleic Acids Res., 21, 3249-55; Chowrira et al., 1994 J. Biol. Chem. 269, 25856).

Such ribozymes are useful for the prevention of the diseases and conditions discussed above, and any other diseases or conditions that are related to the level of CETP activity in a cell or tissue. By "related" is meant 30 that the inhibition of CETP mRNAs and thus reduction in the level of protein activity will relieve to some extent 35 the symptoms of the disease or condition.

Ribozymes are added directly, or can be complexed with cationic lipids, packaged within liposomes, or otherwise delivered to target cells. The nucleic acid or nucleic acid complexes can be locally administered to relevant tissues ex vivo, or in vivo through injection, infusion pump or stent, with or without their incorporation in biopolymers. In preferred embodiments, the ribozymes have binding arms which are complementary to the sequences in Tables II, IV, VI and VII. Examples of such ribozymes are shown in Tables III, V, VI and VII. Examples of such ribozymes consist essentially of sequences defined in these Tables. By "consists essentially of" is meant that the active ribozyme contains an enzymatic center equivalent to those in the examples, and binding arms able to bind mRNA such that cleavage at the target site occurs. Other sequences may be present which do not interfere with such cleavage.

In another aspect of the invention, ribozymes that cleave target molecules and inhibit CETP activity are expressed from transcription units inserted into DNA or RNA vectors. The recombinant vectors are preferably DNA plasmids or viral vectors. Ribozyme expressing viral vectors could be constructed based on, but not limited to, adeno-associated virus, retrovirus, adenovirus, or alphavirus. Preferably, the recombinant vectors capable of expressing the ribozymes are delivered as described above, and persist in target cells. Alternatively, viral vectors may be used that provide for transient expression of ribozymes. Such vectors might be repeatedly administered as necessary. Once expressed, the ribozymes cleave the target mRNA. Delivery of ribozyme expressing vectors could be systemic, such as by intravenous or intramuscular administration, by administration to target cells explanted from the patient followed by reintroduction into the patient, or by any other means that would allow for introduction into the desired target cell.

By "vectors" is meant any nucleic acid- and/or viral-based technique used to deliver a desired nucleic acid.

In a preferred embodiment nucleic acids targeted to Exon 9 of CETP gene is described. A single predominant alternate-splicing variant of the CETP message that lacks exon 9 has been identified and characterized (Inazu et al., 1991 *Biochemistry* 31, 2352; Quinet et al., 1993 *J. Biol. Chem.* 268, 16891). While the function of this abundant splice variant is not clearly understood, it is known to be not secreted and capable of inhibiting secretion of the full-length CETP protein. (Quinet et al. 1993 *J. Biol. Chem.* 16891). Inhibition of full-length CETP secretion is believed to occur due to a heterodimeric complex formation between the full-length and the spliced variant of CETP. This suggests that the spliced variant of CETP might be beneficial in regulating the plasma level of CETP. Nucleic acid-based therapeutics of this invention, therefore, may be selectively targeted to block the expression of exon 9-containing CETP.

Other features and advantages of the invention will be apparent from the following description of the preferred embodiments thereof, and from the claims.

Description Of The Preferred Embodiments

The drawings will first briefly be described.

Drawings

Figure 1 is a diagrammatic representation of the hammerhead ribozyme domain known in the art. Stem II can be ≥ 2 base-pair long.

Figure 2a is a diagrammatic representation of the hammerhead ribozyme domain known in the art; Figure 2b is a diagrammatic representation of the hammerhead ribozyme as divided by Uhlenbeck (1987, *Nature*, 327, 596-600) into a substrate and enzyme portion; Figure 2c is a similar diagram showing the hammerhead divided by Haseloff and Gerlach (1988, *Nature*, 334, 585-591) into two portions;

and Figure 2d is a similar diagram showing the hammerhead divided by Jeffries and Symons (1989, Nucl. Acids. Res., 17, 1371-1371) into two portions.

Figure 3 is a diagrammatic representation of the general structure of a hairpin ribozyme. Helix 2 (H2) is provided with at least 4 base pairs (*i.e.*, n is 1, 2, 3 or 4) and helix 5 can be optionally provided of length 2 or more bases (preferably 3 - 20 bases, *i.e.*, m is from 1 - 20 or more). Helix 2 and helix 5 may be covalently linked by one or more bases (*i.e.*, r is ≥ 1 base). Helix 1, 4 or 5 may also be extended by 2 or more base pairs (*e.g.*, 4 - 20 base pairs) to stabilize the ribozyme structure, and preferably is a protein binding site. In each instance, each N and N' independently is any normal or modified base and each dash represents a potential base-pairing interaction. These nucleotides may be modified at the sugar, base or phosphate. Complete base-pairing is not required in the helices, but is preferred. Helix 1 and 4 can be of any size (*i.e.*, o and p is each independently from 0 to any number, *e.g.*, 20) as long as some base-pairing is maintained. Essential bases are shown as specific bases in the structure, but those in the art will recognize that one or more may be modified chemically (abasic, base, sugar and/or phosphate modifications) or replaced with another base without significant effect. Helix 4 can be formed from two separate molecules, *i.e.*, without a connecting loop. The connecting loop when present may be a ribonucleotide with or without modifications to its base, sugar or phosphate. "q" is ≥ 2 bases. The connecting loop can also be replaced with a non-nucleotide linker molecule. H, refers to bases A, U or C. Y refers to pyrimidine bases.

Figure 4 is a representation of the general structure of the hepatitis delta virus ribozyme domain known in the art.

Figure 5 is a representation of the general structure of the self-cleaving VS RNA ribozyme domain.

Figure 6 is a schematic representation of an RNaseH accessibility assay. Specifically, the left side of Figure 6 is a diagram of complementary DNA oligonucleotides bound to accessible sites on the target RNA.

5 Complementary DNA oligonucleotides are represented by broad lines labeled A, B, and C. Target RNA is represented by the thin, twisted line. The right side of Figure 6 is a schematic of a gel separation of uncut target RNA from a cleaved target RNA. Detection of target

10 RNA is by autoradiography of body-labeled, T7 transcript. The bands common to each lane represent uncleaved target RNA; the bands unique to each lane represent the cleaved products.

Ribozymes

15 Ribozymes of this invention block to some extent CETP production and can be used to treat disease or diagnose such disease. Ribozymes will be delivered to cells in culture and to cells or tissues in animal models of cardiovascular disorders. Ribozyme cleavage of CETP encoded 20 mRNAs in these systems may alleviate disease symptoms.

Target sites

Targets for useful ribozymes can be determined as disclosed in Draper et al., "Method and reagent for treatment of arthritic conditions U.S.S.N. 08/152,487, 25 filed 11/12/93, and hereby incorporated by reference herein in totality. Rather than repeat the guidance provided in those documents here, below are provided specific examples of such methods, not limiting to those in the art. Ribozymes to such targets are designed as 30 described in those applications and synthesized to be tested in vitro and in vivo, as also described.

The sequence of human and rabbit CETP mRNAs were screened for optimal ribozyme target sites using a computer folding algorithm. Hammerhead or hairpin 35 ribozyme cleavage sites were identified. These sites are

shown in Tables II, IV, VI and VII (All sequences are 5' to 3' in the tables) The nucleotide base position is noted in the Tables as that site to be cleaved by the designated type of ribozyme. While rabbit and human sequences can be 5 screened and ribozymes thereafter designed, the human targeted sequences are of most utility. However, as discussed in Stinchcomb et al., "Method and Composition for Treatment of Restenosis and Cancer Using Ribozymes," filed May 18, 1994, U.S.S.N. 08/245,466, rabbit targeted 10 ribozymes may be useful to test efficacy of action of the ribozyme prior to testing in humans. The nucleotide base position is noted in the Tables as that site to be cleaved by the designated type of ribozyme.

Hammerhead or hairpin ribozymes are designed that 15 could bind and were individually analyzed by computer folding (Jaeger et al., 1989 Proc. Natl. Acad. Sci. USA, 86, 7706) to assess whether the ribozyme sequences fold into the appropriate secondary structure. Those ribozymes with unfavorable intramolecular interactions between the 20 binding arms and the catalytic core are eliminated from consideration. Varying binding arm lengths can be chosen to optimize activity. Generally, at least 5 bases on each arm are able to bind to, or otherwise interact with, the target RNA.

Referring to Figure 6, mRNA were screened for accessible cleavage sites by the method described generally in McSwiggen, US Patent application 07/883,849 filed on May 1, 1992, entitled "Assay for ribozyme target site", hereby incorporated by reference herein. Briefly, DNA oligo- 30 nucleotides representing potential hammerhead or hairpin ribozyme cleavage sites were synthesized. A polymerase chain reaction is used to generate substrates for T7 RNA polymerase transcription from human and rabbit CETP cDNA clones. Labeled RNA transcripts are synthesized in vitro 35 from the templates. The oligonucleotides and the labeled transcripts are annealed, RNaseH is added and the mixtures are incubated for the designated times at 37°C. Reactions

are stopped and RNA separated on sequencing polyacrylamide gels. The percentage of the substrate cleaved is determined by autoradiographic quantitation using a PhosphorImaging system. From these data, hammerhead or 5 hairpin ribozyme sites are chosen as the most accessible.

Ribozymes of the hammerhead or hairpin motif are designed to anneal to various sites in the mRNA message. The binding arms are complementary to the target site sequences described above. The ribozymes are chemically 10 synthesized. The method of synthesis used follows the procedure for normal RNA synthesis as described in Usman et al., 1987 J. Am. Chem. Soc., 109, 7845 and in Scaringe et al., 1990 Nucleic Acids Res., 18, 5433 and made use of common nucleic acid protecting and coupling groups, such 15 as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end. The average stepwise coupling yields are >98%. Inactive ribozymes are synthesized by substituting a U for G₅ and a U for A₁₄ (numbering from Hertel et al., 1992 Nucleic Acids Res., 20, 3252). Hairpin ribozymes are 20 synthesized in two parts and annealed to reconstruct the active ribozyme (Chowrira and Burke, 1992 Nucl. Acids. Res., 20, 2835-2840). Ribozymes are also synthesized from DNA templates using bacteriophage T7 RNA polymerase (Milligan and Uhlenbeck, 1989, Methods Enzymol. 180, 51). 25 All ribozymes are modified extensively to enhance stability by modification with nuclease resistant groups, for example, 2'-amino, 2'-C-allyl, 2'-flouro, 2'-O-methyl, 2'-H (for a review see Usman and Cedergren, 1992 TIBS 17, 34). Ribozymes are purified by gel electrophoresis using 30 general methods or are purified by high pressure liquid chromatography (HPLC; See Usman et al., Synthesis, deprotection, analysis and purification of RNA and ribozymes, filed May, 18, 1994, U.S.S.N. 08/245,736 the totality of which is hereby incorporated herein by reference) and are 35 resuspended in water.

The sequences of the ribozymes that are chemically synthesized, useful in this study, are shown in Tables

III, V, VI and VII. Those in the art will recognize that these sequences are representative only of many more such sequences where the enzymatic portion of the ribozyme (all but the binding arms) is altered to affect activity. For example, stem-loop II sequence of hammerhead ribozymes listed in Tables III and V (5'-GGCCGAAAGGCC-3') can be altered (substitution, deletion, and/or insertion) to contain any sequences provided a minimum of two base-paired stem structure can form. Similarly, stem-loop IV sequence of hairpin ribozymes listed in Tables VI and VII (5'-CACGUUGUG-3') can be altered (substitution, deletion, and/or insertion) to contain any sequence, provided a minimum of two base-paired stem structure can form. The sequences listed in Tables III, V, VI and VII may be formed of ribonucleotides or other nucleotides or non-nucleotides. Such ribozymes are equivalent to the ribozymes described specifically in the Tables.

Optimizing Ribozyme Activity

Ribozyme activity can be optimized as described by Stinchcomb et al., *supra*. The details will not be repeated here, but include altering the length of the ribozyme binding arms (stems I and III, see Figure 2c), or chemically synthesizing ribozymes with modifications that prevent their degradation by serum ribonucleases (see e.g., Eckstein et al., International Publication No. WO 92/07065; Perrault et al., 1990 *Nature* 344, 565; Pieken et al., 1991 *Science* 253, 314; Usman and Cedergren, 1992 *Trends in Biochem. Sci.* 17, 334; Usman et al., International Publication No. WO 93/15187; and Rossi et al., International Publication No. WO 91/03162, as well as Usman, N. et al. US Patent Application 07/829,729, and Sproat, European Patent Application 92110298.4 which describe various chemical modifications that can be made to the sugar moieties of enzymatic RNA molecules, modifications which enhance their efficacy in cells, and removal of stem II bases to shorten RNA synthesis times

and reduce chemical requirements. (All these publications are hereby incorporated by reference herein.).

Sullivan, et al., supra, describes the general methods for delivery of enzymatic RNA molecules.

5 Ribozymes may be administered to cells by a variety of methods known to those familiar to the art, including, but not restricted to, encapsulation in liposomes, by iontophoresis, or by incorporation into other vehicles, such as hydrogels, cyclodextrins, biodegradable nanocapsules, and

10 bioadhesive microspheres. For some indications, ribozymes may be directly delivered ex vivo to cells or tissues with or without the aforementioned vehicles. Alternatively, the RNA/vehicle combination is locally delivered by direct injection or by use of a catheter, infusion pump or stent.

15 Other routes of delivery include, but are not limited to, intravascular, intramuscular, subcutaneous or joint injection, aerosol inhalation, oral (tablet or pill form), topical, systemic, ocular, intraperitoneal and/or intrathecal delivery. More detailed descriptions of ribozyme

20 delivery and administration are provided in Sullivan et al., supra and Draper et al., supra which have been incorporated by reference herein.

Another means of accumulating high concentrations of a ribozyme(s) within cells is to incorporate the ribozyme-encoding sequences into a DNA or RNA expression vector.

25 Transcription of the ribozyme sequences are driven from a promoter for eukaryotic RNA polymerase I (pol I), RNA polymerase II (pol II), or RNA polymerase III (pol III). Transcripts from pol II or pol III promoters will be

30 expressed at high levels in all cells; the levels of a given pol II promoter in a given cell type will depend on the nature of the gene regulatory sequences (enhancers, silencers, etc.) present nearby. Prokaryotic RNA polymerase promoters are also used, providing that the prokaryotic RNA polymerase enzyme is expressed in the appropriate

35 cells (Elroy-Stein and Moss, 1990 Proc. Natl. Acad. Sci. USA, 87, 6743-7; Gao and Huang 1993 Nucleic Acids Res.,

21, 2867-72; Lieber et al., 1993 Methods Enzymol., 217,
47-66; Zhou et al., 1990 Mol. Cell. Biol., 10, 4529-37).
Several investigators have demonstrated that ribozymes
expressed from such promoters can function in mammalian
5 cells (e.g. Kashani-Sabet et al., 1992 Antisense Res.
Dev., 2, 3-15; Ojwang et al., 1992 Proc. Natl. Acad. Sci.
USA, 89, 10802-6; Chen et al., 1992 Nucleic Acids Res.,
20, 4581-9; Yu et al., 1993 Proc. Natl. Acad. Sci. USA,
90, 6340-4; L'Huillier et al., 1992 EMBO J. 11, 4411-8;
10 Lisziewicz et al., 1993 Proc. Natl. Acad. Sci. USA, 90,
8000-4). The above ribozyme transcription units can be
incorporated into a variety of vectors for introduction
into mammalian cells, including but not restricted to,
15 plasmid DNA vectors, viral DNA vectors (such as adenovirus
or adeno-associated virus vectors), or viral RNA vectors
(such as retroviral or alphavirus vectors).

In a preferred embodiment of the invention, a trans-
cription unit expressing a ribozyme that cleaves mRNAs
encoded by CETP is inserted into a plasmid DNA vector or
20 an adenovirus or adeno-associated virus DNA viral vector
or a retroviral RNA vector. Viral vectors have been used
to transfer genes and lead to either transient or long
term gene expression (Zabner et al., 1993 Cell 75, 207;
Carter, 1992 Curr. Opin. Biotech. 3, 533). The adenovirus
25 vector is delivered as recombinant adenoviral particles.
The DNA may be delivered alone or complexed with vehicles
(as described for RNA above). The recombinant adenovirus
or AAV particles are locally administered to the site of
treatment, e.g., through incubation or inhalation in vivo
30 or by direct application to cells or tissues ex vivo.

In another preferred embodiments, the ribozyme is
administered to the site of CETP expression (e.g., liver
cells) in an appropriate liposomal vesicle.

Example 1: CETP Hammerhead ribozymes

35 By engineering ribozyme motifs we have designed
several ribozymes directed against CETP encoded mRNA

sequences. These ribozymes are synthesized with modifications that improve their nuclease resistance. The ability of ribozymes to cleave target sequences in vitro was evaluated.

- 5 Several common human cell lines, such as HepG2, are available that can be induced to express endogenous CETP for experimental purposes. Alternatively, non-human cell lines have been developed which constitutively express a cDNA encoding for human CETP (Wang et al., 1991
10 Biochemistry 30, 3484; Wang et al., 1992 J. Biol. Chem. 267, 17487). Additional lines expressing human or rabbit full length or exon 9 deleted cDNA under the control of inducible or constitutive promoters could readily be developed by those skilled in the art. Several rabbit
15 animal models of experimental hypercholesterolemia are available. New Zealand white rabbits fed with high cholesterol diets have been shown to develop atherosclerotic disease (Clarkson et al., 1988 in Use of Animal Models For Research in Human Nutrition, Comparative
20 Animal Nutrition vol. 6, Bexnen and West, eds.) and Watanabe rabbits are a model of homozygous FH (defective LDL receptor) and present with increased cholesterol levels and spontaneous development of atherosclerosis and tendinous xanthomas (Watanabe, 1980 Atherosclerosis 36,
25 261). CETP protein levels can be measured clinically or experimentally by ELISA, or radioimmuno assay. CETP enzyme activity can be measured in vitro or ex vivo by the use of a fluorescently labeled substrate (Bisgaier et al., 1993 J. Lipid Res. 34, 1625; Bisgaier et al., 1994 Lipids
30 29, in press). CETP encoded mRNA levels can be assessed by Northern analysis, RNase protection, primer extension analysis or quantitative RT-PCR. Ribozymes that block the induction of CETP activity and/or CETP protein encoding mRNAs by more than 20% in vitro can be identified.
35 RNA ribozymes and/or genes encoding them will be delivered by either free delivery, liposome delivery, cationic lipid delivery, adeno-associated virus vector

delivery, adenovirus vector delivery, retrovirus vector delivery or plasmid vector delivery in these animal model (e.g., transgenic mouse) experiments. One dose of a ribozyme vector that constitutively expresses the ribozyme or 5 one or more doses of a stable anti-CETP ribozyme or a transiently expressing ribozyme vector may reduce the incidence or severity of atherosclerotic lesions or heart disease.

Diagnostic uses

10 Ribozymes of this invention may be used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of CETP RNA in a cell. The close relationship between ribozyme activity and the structure of the target RNA allows the detection 15 of mutations in any region of the molecule which alters the base-pairing and three-dimensional structure of the target RNA. By using multiple ribozymes described in this invention, one may map nucleotide changes which are important to RNA structure and function *in vitro*, as well 20 as in cells and tissues. Cleavage of target RNAs with ribozymes may be used to inhibit gene expression and define the role (essentially) of specified gene products in the progression of disease. In this manner, other genetic targets may be defined as important mediators of 25 the disease. These experiments will lead to better treatment of the disease progression by affording the possibility of combinational therapies (e.g., multiple ribozymes targeted to different genes, ribozymes coupled with known small molecule inhibitors, or intermittent 30 treatment with combinations of ribozymes and/or other chemical or biological molecules). Other *in vitro* uses of ribozymes of this invention are well known in the art, and include detection of the presence of mRNAs associated with CETP-related condition. Such RNA is detected by 35 determining the presence of a cleavage product after treatment with a ribozyme using standard methodology.

In a specific example, ribozymes which can cleave only wild-type or mutant forms of the target RNA are used for the assay. The first ribozyme is used to identify wild-type RNA present in the sample and the second ribozyme will be used to identify mutant RNA in the sample.

5 As reaction controls, synthetic substrates of both wild-type and mutant RNA will be cleaved by both ribozymes to demonstrate the relative ribozyme efficiencies in the reactions and the absence of cleavage of the "non-targeted" RNA species. The cleavage products from the synthetic substrates will also serve to generate size markers for the analysis of wild-type and mutant RNAs in the sample population. Thus each analysis will require

10 two ribozymes, two substrates and one unknown sample which

15 will be combined into six reactions. The presence of cleavage products will be determined using an RNase protection assay so that full-length and cleavage fragments of each RNA can be analyzed in one lane of a polyacrylamide gel. It is not absolutely required to quantify the

20 results to gain insight into the expression of mutant RNAs and putative risk of the desired phenotypic changes in target cells. The expression of mRNA whose protein product is implicated in the development of the phenotype (*i.e.*, CETP) is adequate to establish risk. If probes of

25 comparable specific activity are used for both transcripts, then a qualitative comparison of RNA levels will be adequate and will decrease the cost of the initial diagnosis. Higher mutant form to wild-type ratios will be correlated with higher risk whether RNA levels are

30 compared qualitatively or quantitatively.

Other embodiments are within the following claims.

Table I

Characteristics of Ribozymes

Group I Introns

Size: ~200 to >1000 nucleotides.

5 Requires a U in the target sequence immediately 5' of the cleavage site.

Binds 4-6 nucleotides at 5'side of cleavage site.

Over 75 known members of this class. Found in Tetrahymena thermophila rRNA, fungal mitochondria, chloroplasts, phage

10 T4, blue-green algae, and others.

RNAseP RNA (M1 RNA)

Size: ~290 to 400 nucleotides.

RNA portion of a ribonucleoprotein enzyme. Cleaves tRNA precursors to form mature tRNA.

15 Roughly 10 known members of this group all are bacterial in origin.

Hammerhead Ribozyme

Size: ~13 to 40 nucleotides.

Requires the target sequence UH immediately 5' of the 20 cleavage site.

Binds a variable number nucleotides on both sides of the cleavage site.

14 known members of this class. Found in a number of plant pathogens (virusoids) that use RNA as the infectious 25 agent (Figure 1)

Hairpin Ribozyme

Size: ~50 nucleotides.

Requires the target sequence GUC immediately 3' of the cleavage site.

30 Binds 4-6 nucleotides at 5'side of the cleavage site and a variable number to the 3'side of the cleavage site.

Only 3 known member of this class. Found in three plant pathogen (satellite RNAs of the tobacco ringspot virus, arabis mosaic virus and chicory yellow mottle virus) which 35 uses RNA as the infectious agent (Figure 3).

Hepatitis Delta Virus (HDV) RibozymeSize: 50 - 60 nucleotides (at present).

- Cleavage of target RNAs recently demonstrated.
Sequence requirements not fully determined.
Binding sites and structural requirements not fully determined, although no sequences 5' of cleavage site are required.
- Only 1 known member of this class. Found in human HDV (Figure 4).
- Neurospora VS RNA Ribozyme
- Size: ~144 nucleotides (at present)
- 10 Cleavage of target RNAs recently demonstrated.
Sequence requirements not fully determined.
Binding sites and structural requirements not fully determined. Only 1 known member of this class. Found in Neurospora VS RNA (Figure 5).

15 Table II: Human CETP HH Target Sequence

	nt.	Sequence	Target Sequence	nt.	Sequence	Target Sequence
	9	UGAAUCU	C UGGGGCC	440	CUCCAUU	C AGAACGU
	45	AGAGCCU	C AUGUUCC	450	AACGUGU	C UGUGGUC
20	50	CUCAUGU	U CCGUGGG	457	CUGUGGU	C UUCAAGG
	51	UCAUGUU	C CGUGGGG	459	GUGGUCU	U CAAGGGG
	72	CGGACAU	A CAUAUAC	460	UGGUCUU	C AAGGGGA
	76	CAUACAU	A UACGGGC	477	CUGAAGU	A UGGCUAC
	78	UACAUUA	A CGGGCUC	483	UAUGGCU	A CACCACU
25	85	ACGGGCU	C CAGGCUG	506	GCUGGGU	A UUGAUCA
	100	AACGGCU	C GGGCCAC	508	UGGGUAU	U GAUCAGU
	109	GGCCACU	U ACACACC	512	UAUUGAU	C AGUCCAU
	110	GCCACTU	A CACACCA	516	GAUCAGU	C CAUUGAC
	127	GCCUGAU	A ACCAUGC	520	AGUCCAU	U GACUUCG
30	148	CCACAGU	C CUGACCC	525	AUUGACU	U CGAGAUC
	186	GCCUGCU	C CAAAGGC	526	UUGACUU	C GAGAUCG
	198	GGCACCU	C GCACGAG	532	UCGAGAU	C GACUCUG
	214	CAGGCAU	C GUGUGCC	537	AUCGACU	C UGCCAUU
	226	GCCGCAU	C ACCAACG	544	CUGCCAU	U GACCUCC
35	241	CUGCCCU	C CUGGUGU	550	UUGACCU	C CAGAUCA
	249	CUGGUGU	U GAACCAC	556	UCCAGAU	C AACACAC

30

	274	AGGUGAU C CAGACCG	579	UGUGACU C UGGUAGA
	285	ACCGCCU U CCAGCGA	584	CUCUGGU A GAGUGCG
	286	CCGCCUU C CAGCGAG	612	GACUGCU A CCUGUCU
	300	GCCAGCU A CCCAGAU	618	UACCUGU C UUUCCAU
5	308	CCCAGAU A UCACGGG	620	CCUGUCU U UCCAUAA
	310	CAGAUAU C ACGGCG	621	CUGUCUU U CCAUAAG
	334	UGAUGCU C CUUGGCC	622	UGUCUUU C CAUAAGC
	337	UGCUCUU U GGCCAAG	626	UUUCCAU A AGCUGCU
	346	GCCAAGU C AAGUAUG	634	AGCUGCU C CUGCAUC
10	351	GUCAAGU A UGGGUUG	641	CCUGCAU C UCCAAGG
	357	UAUGGGU U GCACAAC	643	UGCAUCU C CAAGGGG
	367	ACAACAU C CAGAUCA	670	GGUGGAU C AAGCAGC
	373	UCCAGAU C AGCCACU	681	CAGCUGU U CACAAAU
	381	AGCCACU U GUCCAUC	682	AGCUGUU C ACAAAUU
15	384	CACUUGU C CAUCGCC	689	CACAAAU U UCAUCUC
	388	UGUCCAU C GCCAGCA	690	ACAAAUU U CAUCUCC
	423	GCCAAGU C CAUUGAU	691	CAAAUUU C AUCUCCU
	427	AGUCCAU U GAUGUCU	694	AUUUCAU C UCCUUCA
	433	UUGAUGU C UCCAUUC	696	UUCAUCU C CUUCACC
20	435	GAUGUCU C CAUUCAG	699	AUCUCCU U CACCCUG
	439	UCUCCAU U CAGAACG	700	UCUCCUU C ACCCUGA
	715	AGCUGGU C CUGAAGG	991	GAGUCUU C CACUCGC
	730	GACAGAU C UGCAAAG	996	UUCCACU C GCUGGCC
	742	AAGAGAU C AACGUCA	1009	CCAAGGU A GCUUUCC
25	748	UCAACGU C AUCUCUA	1013	GGUAGCU U UCCAGGA
	751	ACGUCAU C UCUAAC	1014	GUAGCUU U CCAGGAU
	753	GUCAUCU C UAACAUC	1015	UAGCUUU C CAGGAUG
	755	CAUCUCU A ACAUCAU	1030	GCCGCCU C AUGCUCA
	760	CUAACAU C AUGGCCG	1036	UCAUGCU C AGCCUGA
30	770	GGCGGAU U UUGUCCA	1056	GACGAGU U CAAGGCA
	771	GCCGAUU U UGUCCAG	1057	ACGAGUU C AAGGCAG
	772	CCGAUUU U GUCCAGA	1083	UGGGGCU U CAACACC
	775	AUUUUGU C CAGACAA	1084	GGGGCUU C AACACCA
	796	CCAGCAU C CUUUCAG	1102	AGGAAA U UUCCAAAG
35	799	GCAUCCU U UCAGAUG	1104	GAAAUCU U CCAAGAG
	800	CAUCCUU U CAGAUGG	1105	AAAUCUU C CAAGAGG
	801	AUCCUUU C AGAUGGA	1114	AAGAGGU U GUCGGCG

814	GAGACAU U GGGGUGG	1117	AGGUUGU C GGCGCU
826	UGGACAU U UCCCUGA	1125	GGCGCU U CCCCAGC
827	GGACAUU U CCCUGAC	1126	GCGGCUU C CCCAGCC
828	GACAUUU C CCUGACA	1144	CCCAAGU C ACCGUCC
5	842 AGGUGAU C CCGUCAU	1150	UCACCGU C CACUGCC
	847 AUCCCCU C AUCACAG	1159	ACUGCCU C AAGAUGC
	850 CCGUCAU C ACAGCCU	1174	CCAAGAU C UCCUGCC
	858 ACAGCCU C CUACCUG	1176	AAGAUCU C CUGCCAA
	861 GCCUCCU A CCUGGAG	1195	AGGGAGU C GUGGUCA
	10 870 CUGGAGU C CCAUCAC	1201	UCGUGGU C AAUUCUU
	875 GUCCCCAU C ACAAGGG	1205	GGUCAAU U CUUCAGU
	884 CAAGGGU C AUUUCAU	1206	GUCAAUU C UUCAGUG
	887 GGGUCAU U UCAUCUA	1208	CAAUUCU U CAGUGAU
	888 GGUCAUU U CAUCUAC	1209	AAUUCUU C AGUGAUG
15 889 GUCAUUU C AUCUACA	1224	GUGAAA U CCUCUUU	
	892 AUUUCAU C UACAAGA	1225	UGAAAAU C CUCUUUC
	894 UUCAUCU A CAAGAAU	1228	AAUUCCU C UUCCAC
	904 AGAAUGU C UCAGAGG	1230	UUCCUCU U UCCACGC
	906 AAUGUCU C AGAGGAC	1231	UCCUCUU U CCACGCC
20 916 AGGACCU C CCCCUC	1232	CCUCUUU C CACGCC	
	922 UCCCCCU C CCCACCU	1253	GCAACAU U CUGUAGC
	930 CCCACCU U CUCGCC	1254	CAACAUU C UGUAGCU
	931 CCACCUU C UCGCCCA	1258	AUUCUGU A GCUUACA
	933 ACCUUCU C GCCCACA	1262	UGUAGCU U ACACAUU
25 954 GGGGACU C CCGCAUG	1263	GUAGCUU A CACAUUU	
	966 AUGCUGU A CUUCUGG	1269	UACACAU U UGAAGAG
	969 CUGUACU U CUGGUUC	1270	ACACAUU U GAAGAGG
	970 UGUACUU C UGGUUCU	1280	AGAGGAU A UCGUGAC
	975 UUCUGGU U CUCUGAG	1282	AGGAUAU C GUGACUA
30 976 UCUGGUU C UCUGAGC	1289	CGUGACU A CCGUCCA	
	978 UGGUUCU C UGAGCGA	1294	CUACCGU C CAGGCCU
	988 AGCGAGU C UUCCACU	1302	CAGGCCU C CUAUUCU
	990 CGAGUCU U CCACUCG	1305	GCCUCCU A UUCUAAG
	1307 CUCCUAU U CUAAGAA	1569	UUUGGCU U CCCUGAG
35 1308 UCCUAUU C UAAGAAA	1570	UUGGCUU C CCUGAGC	
	1310 CUAUUCU A AGAAAAA	1592	GGUGGAU U UCCUCCA
	1321 AAAAGCU C UUCUUA	1593	GUGGAUU U CCUCCAG

	1323	AAGCUCU U CUUAAGC	1594	UGGAUUU C CUCCAGA
	1324	AGCUCUU C UUAAGCC	1597	AUUUCCU C CAGAGCU
	1326	CUCUUCU U AAGCCUC	1605	CAGAGCU U GAGCUAG
	1327	UCUUCUU A AGCCUCU	1611	UUGAGCU A GAAGUCU
5	1333	UAAGCCU C UUGGAUU	1617	UAGAAGU C UCCAAGG
	1335	AGCCUCU U GGAUUUC	1619	GAAGUCU C CAAGGAG
	1340	CUUGGAU U UCCAGAU	1629	AGGAGGU C GGGAUUGG
	1341	UUGGAUU U CCAGAUU	1641	UGGGGCU U GUAGCAG
	1342	UGGAUUU C CAGAUUA	1644	GGCUTUGU A GCAGAAG
	10 1348	UCCAGAU U ACACCAA	1666	CCAGGCU C ACAGCUG
	1349	CCAGAUU A CACAAA	1686	CUGGUGU C UCCUCCA
	1363	AGACUGU U UCCAACU	1688	GGUGUCU C CUCCAGC
	1364	GACUGUU U CCAACUU	1691	GUCUCCU C CAGCGUG
	1365	ACUGUUU C CAACUUG	1707	UGGAAGU U GGGUUAG
15	1371	UCCAACU U GACUGAG	1712	GUUGGGU U AGGAGUA
	1386	AGCAGCU C CGAGUCC	1713	UUGGGUU A GGAGUAC
	1392	UCCGAGU C CAUCCAG	1719	UAGGAGU A CGGAGAU
	1396	AGUCCAU C CAGAGCU	1733	UGGAGAU U GGCUCCCC
	1404	CAGAGCU U CCUGCAG	1738	AUUGGCU C CCAACUC
	20 1405	AGAGCUU C CUGCAGU	1745	CCCAACU C CUCCUA
	1413	CUGCAGU C AAUGAUC	1748	AACUCCU C CCUAUCC
	1420	CAAUGAU C ACCGCUG	1752	CCUCCCU A UCCUAAA
	1435	UGGGCAU C CCUGAGG	1754	UCCCUAU C CUAAAGG
	1444	CUGAGGU C AUGUCUC	1757	CUAUCCU A AAGGCC
25	1449	GUCAUGU C UCGGCUC	1773	CUGGCAU U AAAGUGC
	1451	CAUGUCU C GGCUCGA	1774	UGGCAUU A AAGUGCU
	1462	UCGAGGU A GGUUUA		
	1467	GUAGUGU U UACAGCC		
	1468	UAGUGUU U ACAGCCC		
	30 1469	AGUGUUU A CAGCCCU		
	1477	CAGCCCU C AUGAACAA		
	1501	UGAGCCU C UUCGACA		
	1503	AGCCUCU U CGACAUC		
	1504	GCCUCUU C GACAUCA		
35	1510	UCGACAU C AUCAACC		
	1513	ACAUCAU C AACCCUG		
	1525	CUGAGAU U AUCACUC		

1526	UGAGAUU A UCACUCG
1528	AGAUUAU C ACUCGAG
1532	UAUCACU C GAGAUGG
1542	GAUGGCCU U CCUGCUG
5 1543	AUGGCUU C CUGCUGC
1563	AUGGACU U UGGCUUC
1564	UGGACUU U GGCUUCC

Table III: Human CETP HH Ribozyme Sequence
nt.

10	<u>Position</u>	<u>HH Ribozyme Sequence</u>
9		GGCCCCA CUGAUGAGGCCGAAAGGCCGAA AGAUUCA
45		GGAACAU CUGAUGAGGCCGAAAGGCCGAA AGGCUCU
50		CCCACGG CUGAUGAGGCCGAAAGGCCGAA ACAUGAG
51		CCCCACG CUGAUGAGGCCGAAAGGCCGAA AACAUAGA
15	72	GUUAUAG CUGAUGAGGCCGAAAGGCCGAA AUGUCCG
	76	GCCCGUA CUGAUGAGGCCGAAAGGCCGAA AUGUAUG
	78	GAGCCCG CUGAUGAGGCCGAAAGGCCGAA AUAUGUA
	85	CAGCCUG CUGAUGAGGCCGAAAGGCCGAA AGCCCGU
	100	GUGGCC CUGAUGAGGCCGAAAGGCCGAA AGCCGUU
20	109	GGUGUGU CUGAUGAGGCCGAAAGGCCGAA AGUGGCC
	110	UGGUGUG CUGAUGAGGCCGAAAGGCCGAA AAGUGGC
	127	GCAUGGU CUGAUGAGGCCGAAAGGCCGAA AUCAGGC
	148	GGGUCAG CUGAUGAGGCCGAAAGGCCGAA ACUGUGG
	186	GCCUUUG CUGAUGAGGCCGAAAGGCCGAA AGCAGGC
25	198	CUCGUGC CUGAUGAGGCCGAAAGGCCGAA AGGUGCC
	214	GGCACAC CUGAUGAGGCCGAAAGGCCGAA AUGCCUG
	226	GCUUGGU CUGAUGAGGCCGAAAGGCCGAA AUGCGGC
	241	ACACCAG CUGAUGAGGCCGAAAGGCCGAA AGGGCAG
	249	GUGGUUC CUGAUGAGGCCGAAAGGCCGAA ACACCAG
30	274	CGGUCUG CUGAUGAGGCCGAAAGGCCGAA AUCACCU
	285	UCGCUGG CUGAUGAGGCCGAAAGGCCGAA AGGCGGU
	286	CUCGCUG CUGAUGAGGCCGAAAGGCCGAA AAGGCAG
	300	AUCUGGG CUGAUGAGGCCGAAAGGCCGAA AGCUGGC
	308	CCCGUGA CUGAUGAGGCCGAAAGGCCGAA AUCUGGG
35	310	CGCCCGU CUGAUGAGGCCGAAAGGCCGAA AUAUCUG
	334	GGCCAAG CUGAUGAGGCCGAAAGGCCGAA AGCAUCA

337 CUUGGCC CUGAUGAGGCCGAAAGGCCGAA AGGAGCA
346 CAUACUU CUGAUGAGGCCGAAAGGCCGAA ACUUGGC
351 CAACCCA CUGAUGAGGCCGAAAGGCCGAA ACUUGAC
357 GUUGUGC CUGAUGAGGCCGAAAGGCCGAA ACCCAUA
5 367 UGAUCUG CUGAUGAGGCCGAAAGGCCGAA AUGUUGU
373 AGUGGCU CUGAUGAGGCCGAAAGGCCGAA AUCUGGA
381 GAUGGAC CUGAUGAGGCCGAAAGGCCGAA AGUGGCU
384 GCGAUG CUGAUGAGGCCGAAAGGCCGAA ACAAGUG
388 UGCUGGC CUGAUGAGGCCGAAAGGCCGAA AUGGACA
10 423 AUCAAUG CUGAUGAGGCCGAAAGGCCGAA ACUUGGC
427 AGACAUC CUGAUGAGGCCGAAAGGCCGAA AUGGACU
433 GAAUGGA CUGAUGAGGCCGAAAGGCCGAA ACAUCAA
435 CUGAAUG CUGAUGAGGCCGAAAGGCCGAA AGACAUC
439 CGUUCUG CUGAUGAGGCCGAAAGGCCGAA AUGGAGA
15 440 ACGUUCU CUGAUGAGGCCGAAAGGCCGAA AAUGGAG
450 GACCACA CUGAUGAGGCCGAAAGGCCGAA ACACGUU
457 CCUGGAA CUGAUGAGGCCGAAAGGCCGAA ACCACAG
459 CCCUUG CUGAUGAGGCCGAAAGGCCGAA AGACCAC
460 UCCCUU CUGAUGAGGCCGAAAGGCCGAA AAGACCA
20 477 GUAGCCA CUGAUGAGGCCGAAAGGCCGAA ACUUCAG
483 AGUGGUG CUGAUGAGGCCGAAAGGCCGAA AGCCAU
506 UGAUCAA CUGAUGAGGCCGAAAGGCCGAA ACCCAGC
508 ACUGAUC CUGAUGAGGCCGAAAGGCCGAA AUACCCA
512 AUGGACU CUGAUGAGGCCGAAAGGCCGAA AUCAAUA
25 516 GUCAAUG CUGAUGAGGCCGAAAGGCCGAA ACUGAUC
520 CGAACUC CUGAUGAGGCCGAAAGGCCGAA AUGGACU
525 GAUCUCG CUGAUGAGGCCGAAAGGCCGAA AGUCAAU
526 CGAUCUC CUGAUGAGGCCGAAAGGCCGAA AAGUCAA
532 CAGAGUC CUGAUGAGGCCGAAAGGCCGAA AUCUCGA
30 537 AAUGGCA CUGAUGAGGCCGAAAGGCCGAA AGUCGAU
544 GGAGGUC CUGAUGAGGCCGAAAGGCCGAA AUGGCAG
550 UGAUCUG CUGAUGAGGCCGAAAGGCCGAA AGGUCAA
556 GUGUGUU CUGAUGAGGCCGAAAGGCCGAA AUCUGGA
579 UCUACCA CUGAUGAGGCCGAAAGGCCGAA AGUCACA
35 584 CGCACUC CUGAUGAGGCCGAAAGGCCGAA ACCAGAG
612 AGACAGG CUGAUGAGGCCGAAAGGCCGAA AGCAGUC
618 AUGGAAA CUGAUGAGGCCGAAAGGCCGAA ACAGGUA

620 UUAUGGA CUGAUGAGGCCGAAAGGCCGAA AGACAGG
621 CUUAUGG CUGAUGAGGCCGAAAGGCCGAA AAGACAG
622 GCUUAUG CUGAUGAGGCCGAAAGGCCGAA AAAGACA
626 AGCAGCU CUGAUGAGGCCGAAAGGCCGAA AUGGAAA
5 634 GAUGCAG CUGAUGAGGCCGAAAGGCCGAA AGCAGCU
641 CCUUGGA CUGAUGAGGCCGAAAGGCCGAA AUGCAGG
643 CCCCUUG CUGAUGAGGCCGAAAGGCCGAA AGAUGCA
670 GCUGCUU CUGAUGAGGCCGAAAGGCCGAA AUCCACC
681 AUUUGUG CUGAUGAGGCCGAAAGGCCGAA ACAGCUG
10 682 AAUUUGU CUGAUGAGGCCGAAAGGCCGAA AACAGCU
689 GAGAUGA CUGAUGAGGCCGAAAGGCCGAA AUUUGUG
690 GGAGAUG CUGAUGAGGCCGAAAGGCCGAA AAUUUGU
691 AGGAGAU CUGAUGAGGCCGAAAGGCCGAA AAAUUUG
694 UGAAGGA CUGAUGAGGCCGAAAGGCCGAA AUGAAAU
15 696 GGUGAAG CUGAUGAGGCCGAAAGGCCGAA AGAUGAA
699 CAGGGUG CUGAUGAGGCCGAAAGGCCGAA AGGAGAU
700 UCAGGGU CUGAUGAGGCCGAAAGGCCGAA AAGGAGA
715 CCUUCAG CUGAUGAGGCCGAAAGGCCGAA ACCAGCU
730 CUUUGCA CUGAUGAGGCCGAAAGGCCGAA AUCUGUC
20 742 UGACGUU CUGAUGAGGCCGAAAGGCCGAA AUCUCUU
748 UAGAGAU CUGAUGAGGCCGAAAGGCCGAA ACGUJGA
751 UGUUAGA CUGAUGAGGCCGAAAGGCCGAA AUGACGU
753 GAUGUUA CUGAUGAGGCCGAAAGGCCGAA AGAUGAC
755 AUGAUGU CUGAUGAGGCCGAAAGGCCGAA AGAGAUG
25 760 CGGCCAU CUGAUGAGGCCGAAAGGCCGAA AUGUUAG
770 UGGACAA CUGAUGAGGCCGAAAGGCCGAA AUCGGCC
771 CUGGACA CUGAUGAGGCCGAAAGGCCGAA AAUCGGC
772 UCUGGAC CUGAUGAGGCCGAAAGGCCGAA AAAUCGG
775 UUGUCUG CUGAUGAGGCCGAAAGGCCGAA ACAAAAU
30 796 CUGAAAG CUGAUGAGGCCGAAAGGCCGAA AUGCUGG
799 CAUCUGA CUGAUGAGGCCGAAAGGCCGAA AGGAUGC
800 CCAUCUG CUGAUGAGGCCGAAAGGCCGAA AAGGAUG
801 UCCAUCU CUGAUGAGGCCGAAAGGCCGAA AAAGGAU
814 CCACCCC CUGAUGAGGCCGAAAGGCCGAA AUGUCUC
35 826 UCAGGGGA CUGAUGAGGCCGAAAGGCCGAA AUGUCCA
827 GUCAGGG CUGAUGAGGCCGAAAGGCCGAA AAUGUCC
828 UGUCAGGG CUGAUGAGGCCGAAAGGCCGAA AAAUGUC

	842	AUGACGG CUGAUGAGGCCGAAAGGCCGAA AUCACCU
	847	CUGUGAU CUGAUGAGGCCGAAAGGCCGAA ACGGGAU
	850	AGGCUGU CUGAUGAGGCCGAAAGGCCGAA AUGACGG
	858	CAGGUAG CUGAUGAGGCCGAAAGGCCGAA AGGCUGU
5	861	CUCCAGG CUGAUGAGGCCGAAAGGCCGAA AGGAGGC
	870	GUGAUGG CUGAUGAGGCCGAAAGGCCGAA ACUCCAG
	875	CCCUUGU CUGAUGAGGCCGAAAGGCCGAA AUGGGAC
	884	AUGAAA U CUGAUGAGGCCGAAAGGCCGAA ACCCUUG
	887	UAGAUGA CUGAUGAGGCCGAAAGGCCGAA AUGACCC
10	888	GUAGAUG CUGAUGAGGCCGAAAGGCCGAA AAUGACC
	889	UGUAGAU CUGAUGAGGCCGAAAGGCCGAA AAAUGAC
	892	UCUUGUA CUGAUGAGGCCGAAAGGCCGAA AUGAAA
	894	AUUCUUG CUGAUGAGGCCGAAAGGCCGAA AGAUGAA
	904	CCUCUGA CUGAUGAGGCCGAAAGGCCGAA ACAUUCU
15	906	GUCCUCU CUGAUGAGGCCGAAAGGCCGAA AGACAUU
	916	GGAGGGG CUGAUGAGGCCGAAAGGCCGAA AGGUCCU
	922	AGGUGGG CUGAUGAGGCCGAAAGGCCGAA AGGGGGA
	930	GGCGAG CUGAUGAGGCCGAAAGGCCGAA AGGUGGG
	931	UGGGCGA CUGAUGAGGCCGAAAGGCCGAA AAGGUGG
20	933	UGUGGGC CUGAUGAGGCCGAAAGGCCGAA AGAAGGU
	954	CAUGC GG CUGAUGAGGCCGAAAGGCCGAA AGUCCCC
	966	CCAGAAC CUGAUGAGGCCGAAAGGCCGAA ACAGCAU
	969	GAACCAG CUGAUGAGGCCGAAAGGCCGAA AGUACAG
	970	AGAACCA CUGAUGAGGCCGAAAGGCCGAA AAGUACA
25	975	CUCAGAG CUGAUGAGGCCGAAAGGCCGAA ACCAGAA
	976	GCUCAGA CUGAUGAGGCCGAAAGGCCGAA AACCGAGA
	978	UCGCUCA CUGAUGAGGCCGAAAGGCCGAA AGAACCA
	988	AGUGGAA CUGAUGAGGCCGAAAGGCCGAA ACUCGCU
	990	CGAGUGG CUGAUGAGGCCGAAAGGCCGAA AGACUCG
30	991	GCGAGUG CUGAUGAGGCCGAAAGGCCGAA AAGACUC
	996	GGCCAGC CUGAUGAGGCCGAAAGGCCGAA AGUGGAA
	1009	GGAAAGC CUGAUGAGGCCGAAAGGCCGAA ACCUUGG
	1013	UCCUGGA CUGAUGAGGCCGAAAGGCCGAA AGCUACC
	1014	AUCCUGG CUGAUGAGGCCGAAAGGCCGAA AAGCUAC
35	1015	CAUCCUG CUGAUGAGGCCGAAAGGCCGAA AAAGCUA
	1030	UGAGCAU CUGAUGAGGCCGAAAGGCCGAA AGCGGC
	1036	UCAGGCU CUGAUGAGGCCGAAAGGCCGAA AGCAUGA

	1056	UGCCUUG CUGAUGAGGCCGAAAGGCCGAA ACUCGUC
	1057	CUGCCUU CUGAUGAGGCCGAAAGGCCGAA AACUCGU
	1083	GGUGUUG CUGAUGAGGCCGAAAGGCCGAA AGCCCCA
	1084	UGGUGUU CUGAUGAGGCCGAAAGGCCGAA AAGCCCC
5	1102	CUUGGAA CUGAUGAGGCCGAAAGGCCGAA AUUUCCU
	1104	CUCUUGG CUGAUGAGGCCGAAAGGCCGAA AGAUUUC
	1105	CCUCUUG CUGAUGAGGCCGAAAGGCCGAA AAGAUUU
	1114	CGCCGAC CUGAUGAGGCCGAAAGGCCGAA ACCUCUU
	1117	AGCCGCC CUGAUGAGGCCGAAAGGCCGAA ACAACCU
10	1125	GCUGGGG CUGAUGAGGCCGAAAGGCCGAA AGCCGCC
	1126	GGCUGGG CUGAUGAGGCCGAAAGGCCGAA AAGCCGC
	1144	GGACGGU CUGAUGAGGCCGAAAGGCCGAA ACUUGGG
	1150	GGCAGUG CUGAUGAGGCCGAAAGGCCGAA ACGGUGA
	1159	GCAUCUU CUGAUGAGGCCGAAAGGCCGAA AGGCAGU
15	1174	GGCAGGA CUGAUGAGGCCGAAAGGCCGAA AUCUUGG
	1176	UUGGCAG CUGAUGAGGCCGAAAGGCCGAA AGAUCUU
	1195	UGACCAC CUGAUGAGGCCGAAAGGCCGAA ACUCCCU
	1201	AAGAAUU CUGAUGAGGCCGAAAGGCCGAA ACCACGA
	1205	ACUGAAC CUGAUGAGGCCGAAAGGCCGAA AUUGACC
20	1206	CACUGAA CUGAUGAGGCCGAAAGGCCGAA AAUUGAC
	1208	AUCACUG CUGAUGAGGCCGAAAGGCCGAA AGAAUUG
	1209	CAUCACU CUGAUGAGGCCGAAAGGCCGAA AAGAAUU
	1224	AAAGAGG CUGAUGAGGCCGAAAGGCCGAA AUUUCAC
	1225	GAAAGAG CUGAUGAGGCCGAAAGGCCGAA AAUUUCA
25	1228	GUGGAAA CUGAUGAGGCCGAAAGGCCGAA AGGAAUU
	1230	GCGUGGA CUGAUGAGGCCGAAAGGCCGAA AGAGGAA
	1231	GGCGUGG CUGAUGAGGCCGAAAGGCCGAA AAGAGGA
	1232	GGGCGUG CUGAUGAGGCCGAAAGGCCGAA AAAGAGG
	1253	GCUACAG CUGAUGAGGCCGAAAGGCCGAA AUGUUGC
30	1254	AGCUACA CUGAUGAGGCCGAAAGGCCGAA AAUGUUG
	1258	UGUAAGC CUGAUGAGGCCGAAAGGCCGAA ACAGAAU
	1262	AAUGUGU CUGAUGAGGCCGAAAGGCCGAA AGCUACA
	1263	AAAUGUG CUGAUGAGGCCGAAAGGCCGAA AAGCUAC
	1269	CUCUUCA CUGAUGAGGCCGAAAGGCCGAA AUGUGUA
35	1270	CCUCUUC CUGAUGAGGCCGAAAGGCCGAA AAUGUGU
	1280	GUCACGA CUGAUGAGGCCGAAAGGCCGAA AUCCUCU
	1282	UAGUCAC CUGAUGAGGCCGAAAGGCCGAA AUAUCCU

	1289	UGGACGG CUGAUGAGGCCGAAAGGCCGAA AGUCACG
	1294	AGGCCUG CUGAUGAGGCCGAAAGGCCGAA ACGGUAG
	1302	AGAAUAG CUGAUGAGGCCGAAAGGCCGAA AGGCCUG
	1305	CUUAGAA CUGAUGAGGCCGAAAGGCCGAA AGGAGGC
5	1307	UUCUUAG CUGAUGAGGCCGAAAGGCCGAA AUAGGAG
	1308	UUUCUUA CUGAUGAGGCCGAAAGGCCGAA AAUAGGA
	1310	UUUUUCU CUGAUGAGGCCGAAAGGCCGAA AGAAUAG
	1321	UUAAGAA CUGAUGAGGCCGAAAGGCCGAA AGCUUUU
	1323	GCUUAAG CUGAUGAGGCCGAAAGGCCGAA AGAGCUU
10	1324	GGCUUAA CUGAUGAGGCCGAAAGGCCGAA AAGAGCU
	1326	GAGGCUU CUGAUGAGGCCGAAAGGCCGAA AGAAGAG
	1327	AGAGGCU CUGAUGAGGCCGAAAGGCCGAA AAGAAGA
	1333	AAUCCAA CUGAUGAGGCCGAAAGGCCGAA AGGCUUA
	1335	GAAAUCC CUGAUGAGGCCGAAAGGCCGAA AGAGGCU
15	1340	AUCUGGA CUGAUGAGGCCGAAAGGCCGAA AUCCAAG
	1341	AAUCUGG CUGAUGAGGCCGAAAGGCCGAA AAUCCAA
	1342	UAAUCUG CUGAUGAGGCCGAAAGGCCGAA AAAUCCA
	1348	UUGGUGU CUGAUGAGGCCGAAAGGCCGAA AUCUGGA
	1349	UUJUGGUG CUGAUGAGGCCGAAAGGCCGAA AAUCUGG
20	1363	AGUUGGA CUGAUGAGGCCGAAAGGCCGAA ACAGUCU
	1364	AAGUUGG CUGAUGAGGCCGAAAGGCCGAA AACAGUC
	1365	CAAGUUG CUGAUGAGGCCGAAAGGCCGAA AAACAGU
	1371	CUCAGUC CUGAUGAGGCCGAAAGGCCGAA AGUUGGA
	1386	GGACUCG CUGAUGAGGCCGAAAGGCCGAA AGCUGCU
25	1392	CUGGAUG CUGAUGAGGCCGAAAGGCCGAA ACUCGGA
	1396	AGCUCUG CUGAUGAGGCCGAAAGGCCGAA AUGGACU
	1404	CUGCAGG CUGAUGAGGCCGAAAGGCCGAA AGCUCUG
	1405	ACUGCAG CUGAUGAGGCCGAAAGGCCGAA AAGCUCU
	1413	GAUCAUU CUGAUGAGGCCGAAAGGCCGAA ACUGCAG
30	1420	CAGCGGU CUGAUGAGGCCGAAAGGCCGAA AUCAUUG
	1435	CCUCAGG CUGAUGAGGCCGAAAGGCCGAA AUGCCCA
	1444	GAGACAU CUGAUGAGGCCGAAAGGCCGAA ACCUCAG
	1449	GAGCCGA CUGAUGAGGCCGAAAGGCCGAA ACAUGAC
	1451	UCGAGCC CUGAUGAGGCCGAAAGGCCGAA AGACAUG
35	1456	CUACCUC CUGAUGAGGCCGAAAGGCCGAA AGCCGAG
	1462	UAAACAC CUGAUGAGGCCGAAAGGCCGAA ACCUCGA
	1467	GGCUGUA CUGAUGAGGCCGAAAGGCCGAA ACACUAC

1468	GGGCUGU CUGAUGAGGCCGAAAGGCCGAA AACACUA
1469	AGGGCUG CUGAUGAGGCCGAAAGGCCGAA AAACACU
1477	UGUUCAU CUGAUGAGGCCGAAAGGCCGAA AGGGCUG
1501	UGUCGAA CUGAUGAGGCCGAAAGGCCGAA AGGCUCA
5 1503	GAUGUCG CUGAUGAGGCCGAAAGGCCGAA AGAGGCU
1504	UGAUGUC CUGAUGAGGCCGAAAGGCCGAA AAGAGGC
1510	GGUUGAU CUGAUGAGGCCGAAAGGCCGAA AUGUCGA
1513	CAGGGUU CUGAUGAGGCCGAAAGGCCGAA AUGAUGU
1525	GAGUGAU CUGAUGAGGCCGAAAGGCCGAA AUCUCAG
10 1526	CGAGGUGA CUGAUGAGGCCGAAAGGCCGAA AAUCUCA
1528	CUCGAGU CUGAUGAGGCCGAAAGGCCGAA AUAAUCU
1532	CCAUCUC CUGAUGAGGCCGAAAGGCCGAA AGUGAUA
1542	CAGCAGG CUGAUGAGGCCGAAAGGCCGAA AGCCAUC
1543	GCAGCAG CUGAUGAGGCCGAAAGGCCGAA AAGCCAU
15 1563	GAAGCCA CUGAUGAGGCCGAAAGGCCGAA AGUCCAU
1564	GGAAGCC CUGAUGAGGCCGAAAGGCCGAA AAGUCCA
1569	CUCAGGG CUGAUGAGGCCGAAAGGCCGAA AGCCAAA
1570	GCUCAGG CUGAUGAGGCCGAAAGGCCGAA AAGCCAA
1592	UGGAGGA CUGAUGAGGCCGAAAGGCCGAA AUCCACC
20 1593	CUGGAGG CUGAUGAGGCCGAAAGGCCGAA AAUCCAC
1594	UCUGGAG CUGAUGAGGCCGAAAGGCCGAA AAAUCCA
1597	AGCUCUG CUGAUGAGGCCGAAAGGCCGAA AGGAAAU
1605	CUAGCUC CUGAUGAGGCCGAAAGGCCGAA AGCUCUG
1611	AGACUUC CUGAUGAGGCCGAAAGGCCGAA AGCUCAA
25 1617	CCUUGGA CUGAUGAGGCCGAAAGGCCGAA ACUUCUA
1619	CUCCUUG CUGAUGAGGCCGAAAGGCCGAA AGACUUC
1629	CCAUCCC CUGAUGAGGCCGAAAGGCCGAA ACCUCCU
1641	CUGCUAC CUGAUGAGGCCGAAAGGCCGAA AGCCCCA
1644	CUUCUGC CUGAUGAGGCCGAAAGGCCGAA ACAAGCC
30 1666	CAGCUGU CUGAUGAGGCCGAAAGGCCGAA AGCCUGG
1686	UGGAGGA CUGAUGAGGCCGAAAGGCCGAA ACACCAG
1688	GCUGGAG CUGAUGAGGCCGAAAGGCCGAA AGACACC
1691	CACGCUG CUGAUGAGGCCGAAAGGCCGAA AGGAGAC
1707	CUAACCC CUGAUGAGGCCGAAAGGCCGAA ACUUCCA
35 1712	UACUCCU CUGAUGAGGCCGAAAGGCCGAA ACCAAC
1713	GUACUCC CUGAUGAGGCCGAAAGGCCGAA AACCCAA
1719	AUCUCCG CUGAUGAGGCCGAAAGGCCGAA ACUCCUA

	1733	GGGAGCC CUGAUGAGGCCGAAAGGCCGAA AUCUCCA
	1738	GAGUUGG CUGAUGAGGCCGAAAGGCCGAA AGCCAAU
	1745	UAGGGAG CUGAUGAGGCCGAAAGGCCGAA AGUUGGG
	1748	GGAUAGG CUGAUGAGGCCGAAAGGCCGAA AGGAGUU
5	1752	UUUAGGA CUGAUGAGGCCGAAAGGCCGAA AGGGAGG
	1754	CCUUUAG CUGAUGAGGCCGAAAGGCCGAA AUAGGGA
	1757	GGGCCUU CUGAUGAGGCCGAAAGGCCGAA AGGAUAG
	1773	GCACUUU CUGAUGAGGCCGAAAGGCCGAA AUGCCAG
	1774	AGCACUU CUGAUGAGGCCGAAAGGCCGAA AAUGCCA

10 Table IV: Rabbit CETP HH Target Sequence

	nt.	nt.		
	<u>Position</u>	<u>Target Sequence</u>	<u>Position</u>	<u>Target Sequence</u>
	20	GGCgCCU C cuACGAG	305	uAcAgcU A cACGaGu
	23	GCCUcCU a CgAgGcu	305	UAcaGCU A CACgAgU
15	23	gccUCCU a CgaggGCU	305	UaCAgCU A CAcGAgU
	36	CuGGCAU C GUGUGuC	323	UGGggGU U GGGcauc
	43	cgUGuGU c GCAucAC	330	UGGGcAU c aAUCAGU
	43	CgUgUgU c gCAUCAc	334	CauCAaU C AGucuGU
	48	GuCGCAU C ACCAACG	334	cAUcaAU C AGUCugU
20	63	CcGCCCU C uUGGUGU	338	aAUCAGU C ugUcGAC
	71	uUGGUGU U GAACCAA	342	AGUCugU c GACUUCG
	96	AGGUGGgU C CAGACgG	342	AgUCUGU c GacUuCg
	96	AGGUGGgU C CaGaCgg	347	gUCGACU U CGAGAUC
	96	AGGuGGU C caGAcGG	348	UcGACUU C GAGAUCG
25	107	ACgGCCU U CCAGCGc	354	UCGAGAU C GACUCUG
	108	CgGCCUU C CAGCGcG	354	UCGaGaU C gAcUCUg
	122	GCCgGCU A uCCgGAc	354	UCGAGAu c GacUcUg
	132	CgGAcgU C AgcGGCG	354	UcGAGAU c GaCUCug
	132	cgGAcGU c agCGGCG	359	AuCgACU c ugCCAuu
30	132	cGGAcGU C aGCGGCG	359	AUCGACU C UGCCAUU
	156	UGAUGCU C CUcGGCC	359	AuCGAcU C UgCCAuu
	159	UGCUCCU c GGCCggG	366	CUGCCAU U GACCUC
	168	GCCggGU C AAGUAcG	372	UUGACCU C CAGAUCA
	168	GccGGGU c AaGuacg	372	UuGAccU C CAGAUcA
35	173	GUCAAGU A cGGGcUG	372	UUGAcCU c cAgaUCa
	189	aCaACcU c CAgAuCA	378	UCCAGAU C AACACAG

189	ACAACcU C CAGAUCA	378	UCCAGAU c AacaCAG
195	UCCAGAU C AGCCACC	378	UCCAgAU c aACacAG
206	CACcUGU C CAUCGCC	434	GACUGCU A CCUGgCU
210	UGUCCAU C GCCAGCA	434	gACUgCU a CCUggCu
5	249 AGaCCAU c GAcGUCg	442	ccUGGcU u UccAUaA
	255 UcGAcGU C gCCAUCc	442	CCUGGCU U UCCAUAA
	261 UCgCCAU c CAGAACG	442	CCUggCU u UCCauAA
	261 ucgCCAU C CAGAaCg	443	CUGgCUU U CCAUAAA
	272 aACgUgU c CGuGgUC	443	CugGcUU u CcauAAA
	10 272 AACGUGU C cGUGGUC	444	uGGcuuU c CAUAAc
	279 CcGUGGU C UUCAAGG	444	UGgCUUU C CAUAAaC
	279 ccGugGU C UuCAAGG	448	UUUCCAU A AaCUGC
	281 GUGGUCU U CAAGGGG	456	AaCUGC U CUGCAC
	282 UGGUCUU C AAGGGGA	465	UGCAcCU C CAgGGGG
15	299 CUGAAcU A cAGCUAC	492	gGUGGCU C aaGcAGc
	299 CuGAaCU a cAGCUAc	492	GGUGGGCU C AAGCAGC
	492 GGUGGCU c aagCAGC	738	AGGcCuU C CCCCUC
	492 gGUgGCCU c AagCAGc	744	UCCCCCU C CgCgCCU
	503 CAGCUCU U CACAAAC	752	CgCgCCU U CcCGCCC
	20 503 CAgcUCU U CACaaAc	752	CGcGcCU u CCcgCCC
	504 aGCucuU c ACAaACu	753	gCgCCUU C cCGCCCg
	504 AGCUCUU C ACAAACU	776	GGGGACU C CCGCAUG
	512 ACAAAcU U CAUCUCC	788	AUGCUCU A CUUCUGG
	513 CAAAcUU C AUCUCCU	791	CUCUACU U CUGGUUC
25	516 AcUUCAU C UCCUUCA	792	UcUACUU C UGGUUCU
	518 UUCAUCU C CUUCACC	797	UUCUGGU U CUCCGAu
	521 AUCUCCU U CACCCUG	798	UCUGGUU C UCcGAuC
	521 aUCUcCU U cAcCCUg	800	UGGUUCU C cGAuCaA
	521 aUCUCCU u CACCcUG	805	CUCcGaU c aAGUGCu
	30 522 UCUCCUU C ACCCUGA	818	cUCaACU C cCUGGCC
	537 AGCUGaU u CUGAAGc	836	GccGCcU U CCAGGAg
	552 GACAGgU C UGCAAuG	836	GcCgccU u cCAGgAG
	552 GaCAGgU C UgCAAUG	837	CcgCCUU c CAGgaGG
	564 AuGAGAU C AACacCA	837	ccGCcUU C CAGGAgG
35	573 ACacCAU C UCCAAC	852	gCCgUCU C GugCuCA
	573 AcacCAU C UcCAAAC	852	GCCGuCU C gUGCUC
	575 acCAUCU C cAACAUc	858	UCgUGCU C AGCCUGA

	582	cCAACaU C AUggCUg	878	GAuGAGU U CAAGaaA
	582	CcAACAU C AUGGCuG	879	AuGAGUU C AAGaaAG
	593	GCuGAcU U UGUCCAG	905	caGGGuU U CgACACC
	594	CuGAcUU U GUCCAGA	906	aGGGuUU C gACACCA
5	597	AcUUUGU C CAGACgA	924	AGGAAA U UUCCAgG
	618	CCAGCAU C CUCUCAG	926	GAAAUCU U CCAgGAG
	621	GCAUCCU c UCAGAUG	926	GAAaUCU u CcAGGAG
	623	AUCCUcU C AGAUGGA	927	AAAUCUU C CAgGAGc
	623	aUccUCU c AGAuggA	936	aGgAGCU U UCCAGag
10	636	GAGACAU c GGGGUGG	937	gGAGCUU u CcagAGg
	648	UGGACAU U UCCgUGA	969	CCcAGGU A GCcgUCC
	649	GGACAUU U CCgUGAC	969	CCCAGGU a gCCGUCC
	650	GACAUUU C CgUGACg	975	UagCCGU C CACUGCC
	650	gAcaUUU C cGUGAcG	984	ACUGCCU u AAGgUGC
15	669	ccCCuGU C AUCACAG	985	cuGCCUU A AgGUGCc
	672	CuGUCAU C ACAGCCa	999	CCAAGAU C UCCUGCC
	672	cuGUCAU c aCAgCcA	1001	AAGAUCU C CUGCCAg
	683	GCCAccU a CcUgGAg	1020	gGGGuGU C GUGGUgu
	683	GCCaCCU A CCUGGAG	1028	gUGGUGU C UuCUuCc
20	692	CuggAgU c cCAUCaC	1030	GGUgucU U CUUCcGU
	692	CUGGAGU C CCAUCAC	1030	GGUGUCU u CUuCcGu
	697	GUCCCCAU C ACAAGGG	1034	UCuUcUU C CGUcGcc
	706	CAAGGGU C AcUUCAc	1049	GUGAcgU U CCgCUUc
	710	GGUCACU U CAcgcAC	1049	gUGaCgU u CcGCUuC
25	711	GUCAcUU C AcgcACA	1050	UGAcgUU C CgCUUcC
	726	AGAAcGU C UCcGAGG	1055	UUCCgCU U cCCcCGC
	728	AAcGUCU C cGAGGcC	1056	UCCgCUU c CCcCGCC
	737	GAGgCcU u CcCcCuC	1088	GUgGCcU A CAggUUU
	1094	UACAggU U UGAgGAG	1408	CGAGauU a uCACUCu
30	1095	ACAggUU U GAgGAGG	1408	cGAGAUU A UCACUCu
	1105	gGAGGAU A UCaUcAC	1410	AGAUUAU C ACUCucG
	1107	AGGAUAU C aUcACcA	1414	UAUCACU C ucGAUGG
	1110	auAUcAU C ACCAcCcG	1445	AUGGACU U cGGuUUu
	1119	CCACcGU C CaGgCCu	1446	UGGACUU c GGuUUuC
35	1119	CcACCGU C CAGGCCU	1451	UUcGGuU U uCCcaAG
	1119	CcAcCgU c cAGGCCu	1452	UcGGuUU u CCcaAGC
	1127	cagGCCU C cUacUCC	1474	GGugGAU U UccUgCA

	1127	CAGGCCU C CUAcUCC	1474	GGUGGAU U UCCUgCA
	1130	GCCUCCU A cUCccAG	1475	GUGGAUU U CCUgCAG
	1133	UCCUAcU C ccAGAAA	1476	UGGAUUU C CUgCAGA
	1146	AAaagCU C UUcCuAC	1529	gACGuCU C cGcCCAu
5	1146	AAAAGCU C UUCcUAc	1529	GAcGUCU C CgcccAu
	1148	AAGCUCU U CcUAcaC	1549	UgGagGU c aGGgagU
	1149	AGCUCUU C cUAcaCC	1580	GAUGGCU c CCaaCUC
	1152	UCUUCCcU A caCCUCU	1580	gaUGGCU C CCAACUC
	1158	UAcaCCU C UUGGAUU	1587	CCCAACU C CUuCugu
	10 1160	caCCUCU U GGAUUUC	1595	CUucUGU c CuGaaGa
	1165	CuUGgAU u UCCAgug	1595	CUuCUGU c CUgAagA
	1165	CUUGGAU U UCCAGug	1595	cuuCUGU C CUgAAGa
	1166	UUGGAUU U CCAAGugc	1624	GCAgCAU a CccUgGg
	1166	UUGGAUU u ccAGUgC	1694	uCcGGaU C cCAGCUG
15	1245	AGgCUGU U UCCAACc	1787	CCuGGCU u uAGcCUG
	1246	GgCUGUU U CCAACcU	1788	CUGGCuU U AgccUGC
	1247	gCuGuuU C CaACCUG	1816	gCuAaAU c UCuCuGG
	1247	gCUGUUU C CAACcUG	1818	UaAAUCU C UcuGGCu
	1247	gcUGUUU c CAaCCug	1818	uAAaucU C UcUgGCU
	20 1268	AGCcGCU C CGAGUCC	1828	UggCUGU C UcUCucU
	1274	UCCGAGU C CcUgCAG	1847	CUcaAGU a AACGAau
	1286	CAGAGCU c uCUcCgc		
	1302	cCCUGAU c gCCAcGg		
	1317	UGGGCAU C CCgGAGG		
25	1326	CgGAGGU C AUGUCUC		
	1331	GUCAUGU C UCGGCUC		
	1333	CAUGUCU C GGCUCGA		
	1338	CUCGGCU C GAGGUgG		
	1349	GuGGCgU u CaCAGCC		
	30 1349	GUgGcGU U cACAGCC		
	1350	UgGcGUU c ACAGCCC		
	1350	UGGcGuU c acAGCcc		
	1359	CAGCCU C AUGAACAA		
	1383	UGgaCCU C UUcGAaaA		
35	1385	gaCCUCU U CGAaAUC		
	1386	aCCUCUU C GAaAUCA		
	1392	UCGAaAU C AUCAACC		

1395 AaAUCAU C AACCCcG
 1407 CcGAGAU U AUCACUC

Table V: Rabbit CETP Hammerhead Ribozyme Sequence
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5	<u>Position</u>	<u>Ribozyme Sequence</u>
	20	CUCGUAG CUGAUGAGGCCGAAAGGCCGAA AGGCGCC
	23	AGCCUCG CUGAUGAGGCCGAAAGGCCGAA AGGAGGC
	23	AGCCUCG CUGAUGAGGCCGAAAGGCCGAA AGGAGGC
	36	GACACAC CUGAUGAGGCCGAAAGGCCGAA AUGCCAG
10	43	GUGAUGC CUGAUGAGGCCGAAAGGCCGAA ACACACG
	43	GUGAUGC CUGAUGAGGCCGAAAGGCCGAA ACACACG
	48	GCUUUGGU CUGAUGAGGCCGAAAGGCCGAA AUGCGAC
	63	ACACCAA CUGAUGAGGCCGAAAGGCCGAA AGGGCGG
	71	UUGGUUC CUGAUGAGGCCGAAAGGCCGAA ACACCAA
15	96	CCGUCUG CUGAUGAGGCCGAAAGGCCGAA ACCACCU
	96	CCGUCUG CUGAUGAGGCCGAAAGGCCGAA ACCACCU
	96	CCGUCUG CUGAUGAGGCCGAAAGGCCGAA ACCACCU
	107	GCGCUGG CUGAUGAGGCCGAAAGGCCGAA AGGCCGU
	108	CGCGCUG CUGAUGAGGCCGAAAGGCCGAA AAGGCCG
20	122	GUCCGGA CUGAUGAGGCCGAAAGGCCGAA AGCCGGC
	132	CGCCGCU CUGAUGAGGCCGAAAGGCCGAA ACCUCCG
	132	CGCCGCU CUGAUGAGGCCGAAAGGCCGAA ACCUCCG
	132	CGCCGCU CUGAUGAGGCCGAAAGGCCGAA ACCUCCG
	156	GGCCGAG CUGAUGAGGCCGAAAGGCCGAA AGCAUCA
25	159	CCCGGCC CUGAUGAGGCCGAAAGGCCGAA AGGAGCA
	168	CGUACUU CUGAUGAGGCCGAAAGGCCGAA ACCCGGC
	168	CGUACUU CUGAUGAGGCCGAAAGGCCGAA ACCCGGC
	173	CAGCCCG CUGAUGAGGCCGAAAGGCCGAA ACUUGAC
	189	UGAUCUG CUGAUGAGGCCGAAAGGCCGAA AGGUUGU
30	189	UGAUCUG CUGAUGAGGCCGAAAGGCCGAA AGGUUGU
	195	GGUGGCU CUGAUGAGGCCGAAAGGCCGAA AUCUGGA
	206	GGCGAUG CUGAUGAGGCCGAAAGGCCGAA ACAGGUG
	210	UGCUGGC CUGAUGAGGCCGAAAGGCCGAA AUGGACA
	249	CGACGUC CUGAUGAGGCCGAAAGGCCGAA AUGGUCU
35	255	GGAUGGC CUGAUGAGGCCGAAAGGCCGAA ACGUCGA
	261	CGUUCUG CUGAUGAGGCCGAAAGGCCGAA AUGGCGA

261 CGUUCUG CUGAUGAGGCCGAAAGGCCGAA AUGGCAG
272 GACCACG CUGAUGAGGCCGAAAGGCCGAA ACACGUU
272 GACCACG CUGAUGAGGCCGAAAGGCCGAA ACACGUU
279 CCUUGAA CUGAUGAGGCCGAAAGGCCGAA ACCACGG
5 279 CCUUGAA CUGAUGAGGCCGAAAGGCCGAA ACCACGG
281 CCCCUUG CUGAUGAGGCCGAAAGGCCGAA AGACCAC
282 UCCCCUU CUGAUGAGGCCGAAAGGCCGAA AAGACCA
299 GUAGCUG CUGAUGAGGCCGAAAGGCCGAA AGUUCAG
299 GUAGCUG CUGAUGAGGCCGAAAGGCCGAA AGUUCAG
10 305 ACUCGUG CUGAUGAGGCCGAAAGGCCGAA AGCUGUA
305 ACUCGUG CUGAUGAGGCCGAAAGGCCGAA AGCUGUA
305 ACUCGUG CUGAUGAGGCCGAAAGGCCGAA AGCUGUA
323 GAUGCCC CUGAUGAGGCCGAAAGGCCGAA ACCCCCCA
330 ACUGAUU CUGAUGAGGCCGAAAGGCCGAA AUGCCCA
15 334 ACAGACU CUGAUGAGGCCGAAAGGCCGAA AUUGAUG
334 ACAGACU CUGAUGAGGCCGAAAGGCCGAA AUUGAUG
338 GUCGACA CUGAUGAGGCCGAAAGGCCGAA ACUGAUU
342 CGAAGUC CUGAUGAGGCCGAAAGGCCGAA ACAGACU
342 CGAAGUC CUGAUGAGGCCGAAAGGCCGAA ACAGACU
20 347 GAUCUCG CUGAUGAGGCCGAAAGGCCGAA AGUCGAC
348 CGAUCUC CUGAUGAGGCCGAAAGGCCGAA AAGUCGA
354 CAGAGUC CUGAUGAGGCCGAAAGGCCGAA AUCUCGA
354 CAGAGUC CUGAUGAGGCCGAAAGGCCGAA AUCUCGA
354 CAGAGUC CUGAUGAGGCCGAAAGGCCGAA AUCUCGA
25 354 CAGAGUC CUGAUGAGGCCGAAAGGCCGAA AUCUCGA
359 AAUGGCA CUGAUGAGGCCGAAAGGCCGAA AGUCGAU
359 AAUGGCA CUGAUGAGGCCGAAAGGCCGAA AGUCGAU
366 GGAGGUC CUGAUGAGGCCGAAAGGCCGAA AUGGCAG
30 372 UGAUCUG CUGAUGAGGCCGAAAGGCCGAA AGGUCAA
372 UGAUCUG CUGAUGAGGCCGAAAGGCCGAA AGGUCAA
372 UGAUCUG CUGAUGAGGCCGAAAGGCCGAA AGGUCAA
378 CUGUGUU CUGAUGAGGCCGAAAGGCCGAA AUCUGGA
378 CUGUGUU CUGAUGAGGCCGAAAGGCCGAA AUCUGGA
35 378 CUGUGUU CUGAUGAGGCCGAAAGGCCGAA AUCUGGA
434 AGCCAGG CUGAUGAGGCCGAAAGGCCGAA AGCAGUC
434 AGCCAGG CUGAUGAGGCCGAAAGGCCGAA AGCAGUC

	442	UUAUGGA CUGAUGAGGCCGAAAGGCCGAA AGCCAGG
	442	UUAUGGA CUGAUGAGGCCGAAAGGCCGAA AGCCAGG
	442	UUAUGGA CUGAUGAGGCCGAAAGGCCGAA AGCCAGG
	443	UUUAUGG CUGAUGAGGCCGAAAGGCCGAA AAGCCAG
5	443	UUUAUGG CUGAUGAGGCCGAAAGGCCGAA AAGCCAG
	444	GUUUUAUG CUGAUGAGGCCGAAAGGCCGAA AAAGCCA
	444	GUUUUAUG CUGAUGAGGCCGAAAGGCCGAA AAAGCCA
	448	AGCAGUU CUGAUGAGGCCGAAAGGCCGAA AUGGAAA
	456	GGUGCAG CUGAUGAGGCCGAAAGGCCGAA AGCAGUU
10	465	CCCCCUG CUGAUGAGGCCGAAAGGCCGAA AGGUGCA
	492	GCUGCUU CUGAUGAGGCCGAAAGGCCGAA AGCCACC
15	503	GUUUGUG CUGAUGAGGCCGAAAGGCCGAA AGAGCUG
	503	GUUUGUG CUGAUGAGGCCGAAAGGCCGAA AGAGCUG
	504	AGUUUUGU CUGAUGAGGCCGAAAGGCCGAA AAGAGCU
	504	AGUUUUGU CUGAUGAGGCCGAAAGGCCGAA AAGAGCU
	512	GGAGAUG CUGAUGAGGCCGAAAGGCCGAA AGUUUGU
20	513	AGGAGAU CUGAUGAGGCCGAAAGGCCGAA AAGUUUG
	516	UGAAGGA CUGAUGAGGCCGAAAGGCCGAA AUGAAGU
	518	GGUGAAG CUGAUGAGGCCGAAAGGCCGAA AGAUGAA
	521	CAGGGUG CUGAUGAGGCCGAAAGGCCGAA AGGAGAU
	521	CAGGGUG CUGAUGAGGCCGAAAGGCCGAA AGGAGAU
25	521	CAGGGUG CUGAUGAGGCCGAAAGGCCGAA AGGAGAU
	522	UCAGGGU CUGAUGAGGCCGAAAGGCCGAA AAGGAGA
	537	GCUUCAG CUGAUGAGGCCGAAAGGCCGAA AUCAGCU
	552	CAUUGCA CUGAUGAGGCCGAAAGGCCGAA ACCUGUC
	552	CAUUGCA CUGAUGAGGCCGAAAGGCCGAA ACCUGUC
30	564	UGGUGUU CUGAUGAGGCCGAAAGGCCGAA AUCUCAU
	573	UGUUGGA CUGAUGAGGCCGAAAGGCCGAA AUGGUGU
	573	UGUUGGA CUGAUGAGGCCGAAAGGCCGAA AUGGUGU
	575	GAUGUUG CUGAUGAGGCCGAAAGGCCGAA AGAUGGU
	582	CAGCCAU CUGAUGAGGCCGAAAGGCCGAA AUGUUGG
35	582	CAGCCAU CUGAUGAGGCCGAAAGGCCGAA AUGUUGG
	593	CUGGACA CUGAUGAGGCCGAAAGGCCGAA AGUCAGC
	594	UCUGGAC CUGAUGAGGCCGAAAGGCCGAA AAGUCAG

597 UCGUCUG CUGAUGAGGCCGAAAGGCCGAA ACAAAGU
618 CUGAGAG CUGAUGAGGCCGAAAGGCCGAA AUGCUGG
621 CAUCUGA CUGAUGAGGCCGAAAGGCCGAA AGGAUGC
623 UCCAUCU CUGAUGAGGCCGAAAGGCCGAA AGAGGAU
5 623 UCCAUCU CUGAUGAGGCCGAAAGGCCGAA AGAGGAU
636 CCACCCC CUGAUGAGGCCGAAAGGCCGAA AUGUCUC
648 UCACGGA CUGAUGAGGCCGAAAGGCCGAA AUGUCCA
649 GUCACGG CUGAUGAGGCCGAAAGGCCGAA AAUGUCC
650 CGUCACG CUGAUGAGGCCGAAAGGCCGAA AAAUGUC
10 650 CGUCACG CUGAUGAGGCCGAAAGGCCGAA AAAUGUC
669 CUGUGAU CUGAUGAGGCCGAAAGGCCGAA ACAGGGG
672 UGGCUGU CUGAUGAGGCCGAAAGGCCGAA AUGACAG
672 UGGCUGU CUGAUGAGGCCGAAAGGCCGAA AUGACAG
683 CUCCAGG CUGAUGAGGCCGAAAGGCCGAA AGGUGGC
15 683 CUCCAGG CUGAUGAGGCCGAAAGGCCGAA AGGUGGC
692 GUGAUGG CUGAUGAGGCCGAAAGGCCGAA ACUCCAG
692 GUGAUGG CUGAUGAGGCCGAAAGGCCGAA ACUCCAG
697 CCCUUGU CUGAUGAGGCCGAAAGGCCGAA AUGGGAC
706 GUGAAGU CUGAUGAGGCCGAAAGGCCGAA ACCCUUG
20 710 GUGCGUG CUGAUGAGGCCGAAAGGCCGAA AGUGACC
711 UGUGCUG CUGAUGAGGCCGAAAGGCCGAA AAGUGAC
726 CCUCGGA CUGAUGAGGCCGAAAGGCCGAA ACGUUCU
728 GGCCUCG CUGAUGAGGCCGAAAGGCCGAA AGACGUU
737 GAGGGGG CUGAUGAGGCCGAAAGGCCGAA AGGCCUC
25 738 GGAGGGG CUGAUGAGGCCGAAAGGCCGAA AAGGCCU
744 AGGCGCG CUGAUGAGGCCGAAAGGCCGAA AGGGGGA
752 GGGCGGG CUGAUGAGGCCGAAAGGCCGAA AGGCGCG
752 GGGCGGG CUGAUGAGGCCGAAAGGCCGAA AGGCGCG
753 CGGGCGG CUGAUGAGGCCGAAAGGCCGAA AAGGCGC
30 776 CAUGCGG CUGAUGAGGCCGAAAGGCCGAA AGUCCCC
788 CCAGAAC CUGAUGAGGCCGAAAGGCCGAA AGAGCAU
791 GAACCAG CUGAUGAGGCCGAAAGGCCGAA AGUAGAG
792 AGAACCA CUGAUGAGGCCGAAAGGCCGAA AAGUAGA
797 AUCGGAG CUGAUGAGGCCGAAAGGCCGAA ACCAGAA
35 798 GAUCGGA CUGAUGAGGCCGAAAGGCCGAA AACCCAGA
800 UUGAUUC CUGAUGAGGCCGAAAGGCCGAA AGAACCA
805 AGCACUU CUGAUGAGGCCGAAAGGCCGAA AUCGGAG

	818	GGCCAGG CUGAUGAGGCCGAAAGGCCGAA AGUUGAG
	836	CUCCUGG CUGAUGAGGCCGAAAGGCCGAA AGGCCGC
	836	CUCCUGG CUGAUGAGGCCGAAAGGCCGAA AGGCCGC
	837	CCUCCUG CUGAUGAGGCCGAAAGGCCGAA AAGGCCG
5	837	CCUCCUG CUGAUGAGGCCGAAAGGCCGAA AAGGCCG
	852	UGAGCAC CUGAUGAGGCCGAAAGGCCGAA AGACGGC
	852	UGAGCAC CUGAUGAGGCCGAAAGGCCGAA AGACGGC
	858	UCAGGCU CUGAUGAGGCCGAAAGGCCGAA AGCACGA
	878	UUUCUUG CUGAUGAGGCCGAAAGGCCGAA ACUCAUC
10	879	CUUUCUU CUGAUGAGGCCGAAAGGCCGAA AACUCAU
	905	GGUGUCG CUGAUGAGGCCGAAAGGCCGAA AACCCUG
	906	UGGUGUC CUGAUGAGGCCGAAAGGCCGAA AAACCCU
	924	CCUGGAA CUGAUGAGGCCGAAAGGCCGAA AUUUCCU
	926	CUCCUGG CUGAUGAGGCCGAAAGGCCGAA AGAUUUC
15	926	CUCCUGG CUGAUGAGGCCGAAAGGCCGAA AGAUUUC
	927	GCUCCUG CUGAUGAGGCCGAAAGGCCGAA AAGAUUU
	936	CUCUGGA CUGAUGAGGCCGAAAGGCCGAA AGCUCCU
	937	CCUCUGG CUGAUGAGGCCGAAAGGCCGAA AAGCUCC
	969	GGACGGC CUGAUGAGGCCGAAAGGCCGAA ACCUGGG
20	969	GGACGGC CUGAUGAGGCCGAAAGGCCGAA ACCUGGG
	975	GGCAGUG CUGAUGAGGCCGAAAGGCCGAA ACGGCUA
	984	GCACCUU CUGAUGAGGCCGAAAGGCCGAA AGGCAGU
	985	GGCACCU CUGAUGAGGCCGAAAGGCCGAA AAGGCAG
	999	GGCAGGA CUGAUGAGGCCGAAAGGCCGAA AUCUUGG
25	1001	CUGGCAG CUGAUGAGGCCGAAAGGCCGAA AGAUCUU
	1020	ACACCAC CUGAUGAGGCCGAAAGGCCGAA ACACCCC
	1028	GGAAGAA CUGAUGAGGCCGAAAGGCCGAA ACACCAC
	1030	ACGGAAG CUGAUGAGGCCGAAAGGCCGAA AGACACC
	1030	ACGGAAG CUGAUGAGGCCGAAAGGCCGAA AGACACC
30	1034	GGCGACG CUGAUGAGGCCGAAAGGCCGAA AAGAAGA
	1049	GAAGCGG CUGAUGAGGCCGAAAGGCCGAA ACGUCAC
	1049	GAAGCGG CUGAUGAGGCCGAAAGGCCGAA ACGUCAC
	1050	GGAAGCG CUGAUGAGGCCGAAAGGCCGAA AACGUCA
	1055	GCGGGGG CUGAUGAGGCCGAAAGGCCGAA AGCGGAA
35	1056	GGCGGGGG CUGAUGAGGCCGAAAGGCCGAA AAGCGGA
	1088	AAACCUG CUGAUGAGGCCGAAAGGCCGAA AGGCCAC
	1094	CUCCUCA CUGAUGAGGCCGAAAGGCCGAA ACCUGUA

1095 CCUCCUC CUGAUGAGGCCGAAAGGCCGAA AACCUGU
 1105 GUGAUGA CUGAUGAGGCCGAAAGGCCGAA AUCCUCC
 1107 UGGUGAU CUGAUGAGGCCGAAAGGCCGAA AUAUCCU
 1110 CGGUGGU CUGAUGAGGCCGAAAGGCCGAA AUGAUAU
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 30 1286 GCGGAGA CUGAUGAGGCCGAAAGGCCGAA AGCUCUG
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 1317 CCUCCGG CUGAUGAGGCCGAAAGGCCGAA AUGCCCA
 1326 GAGACAU CUGAUGAGGCCGAAAGGCCGAA ACCUCCG
 35 1331 GAGCCGA CUGAUGAGGCCGAAAGGCCGAA ACAUGAC
 1333 UCGAGCC CUGAUGAGGCCGAAAGGCCGAA AGACAUG
 1338 CCACCUC CUGAUGAGGCCGAAAGGCCGAA AGCCGAG

	1349	GGCUGUG CUGAUGAGGCCGAAAGGCCGAA ACGCCAC
	1349	GGCUGUG CUGAUGAGGCCGAAAGGCCGAA ACGCCAC
	1350	GGGCUGU CUGAUGAGGCCGAAAGGCCGAA AACGCCA
	1350	GGGCUGU CUGAUGAGGCCGAAAGGCCGAA AACGCCA
5	1359	UGUUCAU CUGAUGAGGCCGAAAGGCCGAA AGGGCUG
	1383	UUUCGAA CUGAUGAGGCCGAAAGGCCGAA AGGUCCA
	1385	GAUUUCG CUGAUGAGGCCGAAAGGCCGAA AGAGGUC
	1386	UGAUUUC CUGAUGAGGCCGAAAGGCCGAA AAGAGGU
	1392	GGUUGAU CUGAUGAGGCCGAAAGGCCGAA AUUUCGA
10	1395	CGGGGUU CUGAUGAGGCCGAAAGGCCGAA AUGAUUU
	1407	GAGUGAU CUGAUGAGGCCGAAAGGCCGAA AUCUCGG
	1408	AGAGUGA CUGAUGAGGCCGAAAGGCCGAA AAUCUCG
	1408	AGAGUGA CUGAUGAGGCCGAAAGGCCGAA AAUCUCG
	1410	CGAGAGU CUGAUGAGGCCGAAAGGCCGAA AUAAUCU
15	1414	CCAUCGA CUGAUGAGGCCGAAAGGCCGAA AGUGAUA
	1445	AAAACCG CUGAUGAGGCCGAAAGGCCGAA AGUCCAU
	1446	GAAAACC CUGAUGAGGCCGAAAGGCCGAA AAGUCCA
	1451	CUUGGGA CUGAUGAGGCCGAAAGGCCGAA AACCGAA
	1452	GCUUGGG CUGAUGAGGCCGAAAGGCCGAA AAACCGA
20	1474	UGCAGGA CUGAUGAGGCCGAAAGGCCGAA AUCCACC
	1474	UGCAGGA CUGAUGAGGCCGAAAGGCCGAA AUCCACC
	1475	CUGCAGG CUGAUGAGGCCGAAAGGCCGAA AAUCCAC
	1476	UCUGCAG CUGAUGAGGCCGAAAGGCCGAA AAAUCCA
	1529	AUGGGCG CUGAUGAGGCCGAAAGGCCGAA AGACGUC
25	1529	AUGGGCG CUGAUGAGGCCGAAAGGCCGAA AGACGUC
	1549	ACUCCCCU CUGAUGAGGCCGAAAGGCCGAA ACCUCCA
	1580	GAGUUGG CUGAUGAGGCCGAAAGGCCGAA AGCCAUC
	1580	GAGUUGG CUGAUGAGGCCGAAAGGCCGAA AGCCAUC
	1587	ACAGAAC CUGAUGAGGCCGAAAGGCCGAA AGUUGGG
30	1595	UCUUCAG CUGAUGAGGCCGAAAGGCCGAA ACAGAAC
	1595	UCUUCAG CUGAUGAGGCCGAAAGGCCGAA ACAGAAC
	1595	UCUUCAG CUGAUGAGGCCGAAAGGCCGAA ACAGAAC
	1624	CCCAGGG CUGAUGAGGCCGAAAGGCCGAA AUGCUGC
	1694	CAGCUGG CUGAUGAGGCCGAAAGGCCGAA AUCCGGA
35	1787	CAGGCUA CUGAUGAGGCCGAAAGGCCGAA AGCCAGG
	1788	GCAGGCU CUGAUGAGGCCGAAAGGCCGAA AAGCCAG
	1816	CCAGAGA CUGAUGAGGCCGAAAGGCCGAA AUUUAGC

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1818 AGCCAGA CUGAUGAGGCCGAAAGGCCGAA AGAUUUA
1818 AGCCAGA CUGAUGAGGCCGAAAGGCCGAA AGAUUUA
1828 AGAGAGA CUGAUGAGGCCGAAAGGCCGAA ACAGCCA
1847 AUUCGUU CUGAUGAGGCCGAAAGGCCGAA ACUUGAG

Table VI: Human CETP Hairpin Ribozyme and Substrate Sequence

nt.	Position	Ribozyme Sequence	Substrate
	27	UUCGGGG AGAA GGGUCU ACCAGAGAAAACACGUTUGGUACAUUACUGGU	AGACCU GCU GCCCCGAA
5	30	CUCUCCG AGAA GCAGGG ACCAGAGAAAACACGUTUGGUACAUUACUGGU	CCCUGCU GCC CGGAAGAG
96	96	GUGGCCG AGAA GUUCAG ACCAGAGAAAACACGUTUGGUACAUUACUGGU	CUGAACG GCU CGGCCAC
119	GGUUAUCA	AGAA GUGGUG ACCAGAGAAAACACGUTUGGUACAUUACUGGU	CACCAU GCU UGUAUACC
145	AGGGUCAG	AGAA GUGGCA ACCAGAGAAAACACGUTUGGUACAUUACUGGU	UGCCACA GUC CUGACCTU
150	GGGCCAGG	AGAA GGACUG ACCAGAGAAAACACGUTUGGUACAUUACUGGU	CAGUCCU GAC CCUGGCC
162	162	CAUUGCCC AGAA GGGCCA ACCAGAGAAAACACGUTUGGUACAUUACUGGU	UGGCCU GCU GGGCAAUG
182	GCCUTUGG	AGAA GGCAUG ACCAGAGAAAACACGUTUGGUACAUUACUGGU	CAUGCCU GCU CCAAAGGC
235	ACCAGGAG	AGAA GGGCUTG ACCAGAGAAAACACGUTUGGUACAUUACUGGU	CAAGCCU GCC CUCCUGGU
276	GGAAAGGGC	AGAA GGAUCA ACCAGAGAAAACACGUTUGGUACAUUACUGGU	UGAUCCA GAC CGCCUTCC
280	CGCUGGAA	AGAA GUCUGC ACCAGAGAAAACACGUTUGGUACAUUACUGGU	CCAGACC GCC UUCCAGCG
369	AGUGGGUG	AGAA GGAGUU ACCAGAGAAAACACGUTUGGUACAUUACUGGU	ACAUCCA GAU CAGCCACU
490	AGCCACCA	AGAA GUGGUG ACCAGAGAAAACACGUTUGGUACAUUACUGGU	CACCAU GCC UGGUGGGU
513	AGUCAAUG	AGAA GAUCAA ACCAGAGAAAACACGUTUGGUACAUUACUGGU	UUGAUCA GUC CAUGACU
552	GUGGUUG	AGAA GGAGGU ACCAGAGAAAACACGUTUGGUACAUUACUGGU	ACCUCCA GAU CAACACAC
564	CACAGGU	AGAA GUGGU ACCAGAGAAAACACGUTUGGUACAUUACUGGU	ACACACA GCU GACCUUGUG
20	567	AGUCACAG AGAA GCUGUG ACCAGAGAAAACACGUTUGGUACAUUACUGGU	CACAGCU GAC CUGUGACU

591	GGGCAUCG AGAA GCACUC ACCAGAGAAAACACAGTUGGGUACAUUACCUGGU	GAGIUGCG GAC CGAUGCCC
595	UCAGGGGC AGAA GUCCGC ACCAGAGAAAACACAGTUGGGUACAUUACCUGGU	GCGGACCC GAU GCCCCUGA
604	AGGUAGCA AGAA GGGGCA ACCAGAGAAAACACAGTUGGGUACAUUACCUGGU	UGCCCTU GAC UGCUACCU
615	UAUGGAAA AGAA GGUGAC ACCAGAGAAAACACAGTUGGGUACAUUACCUGGU	GCUACCU GUC UUUCCAUU
5	630 GAUGGAGG AGAA GCUUUAU ACCAGAGAAAACACAGTUGGGUACAUUACCUGGU	AUAAGCU GCU CCUGCAUC
675	UUGUGAAC AGAA GCUUGA ACCAGAGAAAACACAGTUGGGUACAUUACCUGGU	UCAAGCA GCU GUUCACAA
678	AAUTUGUG AGAA GCUGCU ACCAGAGAAAACACAGTUGGGUACAUUACCUGGU	AGCAGCU GUT CACAAAUU
726	CUTUGGAG AGAA GUCCCCU ACCAGAGAAAACACAGTUGGGUACAUUACCUGGU	AGGGACA GAU CUGCAAAG
766	UGGACAAA AGAA GCCAUG ACCAGAGAAAACACAGTUGGGUACAUUACCUGGU	CAUGGCC GAU UUUGUCCA
10	802 AUGUCUCC AGAA GAAAGG ACCAGAGAAAACACAGTUGGGUACAUUACCUGGU	CCUUUCA GAU GGAGACAU
853	AGGUAGGA AGAA GUGAUG ACCAGAGAAAACACAGTUGGGUACAUUACCUGGU	CAUCACA GCC UCCUACCU
942	AGUCCCCC AGAA GUGUGG ACCAGAGAAAACACAGTUGGGUACAUUACCUGGU	CCACACU GCU GGGGGACU
1025	GAGCAUGA AGAA GCCAUC ACCAGAGAAAACACAGTUGGGUACAUUACCUGGU	GAUGGCC GCC UCAUGGTC
1037	UCCCAUCA AGAA GAGCAU ACCAGAGAAAACACAGTUGGGUACAUUACCUGGU	AUGCUCA GCC UGAUGGGA
15	1041 CGUCUCCC AGAA GGGCUA ACCAGAGAAAACACAGTUGGGUACAUUACCUGGU	UCAGCCU GAU GGGAGACG
1121	GCUGGGGA AGAA GCCGAC ACCAGAGAAAACACAGTUGGGUACAUUACCUGGU	GUCCGGCG GCU UCCCCAGC
1147	AGGCAGUG AGAA GUGACU ACCAGAGAAAACACAGTUGGGUACAUUACCUGGU	AGUCACC GUC CACUGCCU
1154	CAUCUUGA AGAA GUGGAC ACCAGAGAAAACACAGTUGGGUACAUUACCUGGU	GUCCACU GCC UCAAGAUG
1240	UGUUGCTUG AGAA GGGCGU ACCAGAGAAAACACAGTUGGGUACAUUACCUGGU	ACGCCCA GAC CAGCAACA
20	1291 GAGGCCCTUG AGAA GUAGUC ACCAGAGAAAACACAGTUGGGUACAUUACCUGGU	GACTUACC GUC CAGGCCUC

1344	UGGGUGUA AGAA GGAAAU ACCAGAGAACACACGUTUGGUUACAUUACUGGU	AUUCCA GAU UACACCAA
1360	AAGUTGGA AGAA GUCUUU ACCAGAGAACACACGUTUGGUUACAUUACUGGU	AAAGACU GUU UCCAACUU
1382	GGACUCGG AGAA GCUCUC ACCAGAGAACACACGUTUGGUUACAUUACUGGU	GAGAGCA GCU CCGAGUCC
1423	AUGCCCAC AGAA GUGAUC ACCAGAGAACACACGUTUGGUUACAUUACUGGU	GAUCACC GCU GUGGGCAU
5 1452	CUACCU CG AGAA GAGACA ACCAGAGAACACACGUTUGGUUACAUUACUGGU	UGUCUCG GCU CGAGGUAG
1471	UUCAUGAG AGAA GUAAAC ACCAGAGAACACACGUTUGGUUACAUUACUGGU	GUUUACA GCC CUCAUGAA
1545	UCUGGAGC AGAA GGAAGC ACCAGAGAACACACGUTUGGUUACAUUACUGGU	GCUUCCU GCU GCUGGAGA
1548	CCAUCUGC AGAA GCAGGA ACCAGAGAACACACGUTUGGUUACAUUACUGGU	UCCUGCU GCU GCAGAUCC
1554	CAAAGUCC AGAA GCAGCA ACCAGAGAACACACGUTUGGUUACAUUACUGGU	UGCUGCA GAU GGACTTUG
10 1581	AAUCCACC AGAA GGUGCU ACCAGAGAACACACGUTUGGUUACAUUACUGGU	AGCACCU GCU GGUGGAU
1669	AGGGUTUCC AGAA GUGAGC ACCAGAGAACACACGUTUGGUUACAUUACUGGU	GCUCACA GCU GGAACCCU

Table VII: Rabbit CETP Hairpin Ribozyme and Substrate Sequences

nt.	Position	Ribozyme Sequence	Substrate
15	57	ACCAAGAG AGAA GGCUTUG ACCAGAGAACACACGUTUGGUUACAUUACUGGU	CAAGCCC GCC CUCUUGGU
98		GGAAAGGCC AGAA GGACCA ACCAGAGAACACACGUTUGGUUACAUUACUGGU	UGGUCCA GAC GGCCUCC
102		CGCUGGAA AGAA GUCUGG ACCAGAGAACACACGUTUGGUUACAUUACUGGU	CCAGACG GCC UUCCAGCG
126		CCGCUGAC AGAA GGAAUAG ACCAGAGAACACACGUTUGGUUACAUUACUGGU	CUAUCCG GAC GUCAGGG
160		CUUGACCC AGAA GAGGAG ACCAGAGAACACACGUTUGGUUACAUUACUGGU	CUCUCG GCC GGGUCAAG

191	GGUGGCGU	AGAA	GGAGGU	ACCAGAGAAACACAGUTUGGGUACAUUACUGGU	ACCUCCA	GAU	CAGGCCACC	
203	UGGCGAUG	AGAA	GGUGGC	ACCAGAGAAACACAGUTUGGGUACAUUACUGGU	GCCACCU	GUC	CAUCGCCA	
335	AGUCGACA	AGAA	GAUUGA	ACCAGAGAAACACAGUTUGGGUACAUUACUGGU	UCAAUCA	GUC	UGUGGACU	
339	UCGAAGUC	AGAA	GACUGA	ACCAGAGAAACACAGUTUGGGUACAUUACUGGU	UCAGUTU	GUC	GACUUCGA	
5	374	CUGUGUG	AGAA	GGAGGU	ACCAGAGAAACACAGUTUGGGUACAUUACUGGU	ACCUCCA	GAU	CAACACAG
389	CGUCGCA	AGAA	GCUCUG	ACCAGAGAAACACAGUTUGGGUACAUUACUGGU	CAGAGCU	GAC	CUGCGAGC	
426	AGGUAGCA	AGAA	GGGGCA	ACCAGAGAAACACAGUTUGGGUACAUUACUGGU	UGCCCCC	GAC	UGCUACCU	
452	GGUGCAGG	AGAA	GUUUAU	ACCAGAGAAACACAGUTUGGGUACAUUACUGGU	AUAAGCU	GCU	CCUGGCAC	
497	UUGUGAAG	AGAA	GCUGUA	ACCAGAGAAACACAGUTUGGGUACAUUACUGGU	UCAAGCA	GCU	CUUCACAA	
10	533	GUUCAGA	AGAA	GCUUUCA	ACCAGAGAAACACAGUTUGGGUACAUUACUGGU	UGAAGCU	GAU	UCUGAACG
588	UGGACAAA	AGAA	GCCAUG	ACCAGAGAAACACAGUTUGGGUACAUUACUGGU	CAUGGCU	GAC	UUTUGUCCA	
599	CGGCCUC	AGAA	GGACAA	ACCAGAGAAACACAGUTUGGGUACAUUACUGGU	UUGUCCA	GAC	GAGGGCCG	
624	AUGUCUCC	AGAA	GAGAGG	ACCAGAGAAACACAGUTUGGGUACAUUACUGGU	CCUCUCA	GAU	GGAGACAU	
755	GAAGACCG	AGAA	GGAAAGG	ACCAGAGAAACACAGUTUGGGUACAUUACUGGU	CCUUCCC	GCC	CGGUCTUC	
15	760	CCCCAGAA	AGAA	GGGGGG	ACCAGAGAAACACAGUTUGGGUACAUUACUGGU	CCGCCCC	GUC	UUCUGGG
801	AGCACUUG	AGAA	GAGAAC	ACCAGAGAAACACAGUTUGGGUACAUUACUGGU	GTUCUCC	GAU	CAAGUGCU	
831	UCCUGGAA	AGAA	GCCCCUG	ACCAGAGAAACACAGUTUGGGUACAUUACUGGU	CAGGGCC	GCC	UUCAGGGA	
847	GAGGCCGA	AGAA	GCCCCUC	ACCAGAGAAACACAGUTUGGGUACAUUACUGGU	GAGGGCC	GUC	UCGUGGUC	
859	CCCUGUCA	AGAA	GAGCAC	ACCAGAGAAACACAGUTUGGGUACAUUACUGGU	GUGCUCA	GCC	UGACAGGG	
20	972	AGGCAGUG	AGAA	GCUCUCC	ACCAGAGAAACACAGUTUGGGUACAUUACUGGU	GGUAGCC	GUC	CAUCGCU

979	CACCUUAA AGAA GUCCGAC ACCAGAGAAAACACACGUUGGGUACAUUACCUGGU	GUCCACU GCC UUAAGGGU
1035	GUCACGGC AGAA GAAGAA ACCAGAGAAAACACACGUUGGGUACAUUACCUGGU	UUCUTCC GUC GCGGUGAC
1051	GGGGGGGA AGAA GAACGU ACCAGAGAAAACACACGUUGGGUACAUUACCUGGU	ACGTUCC GCU UCCCCCGC
1060	GCCAUCUG AGAA GGGGAA ACCAGAGAAAACACACGUUGGGUACAUUACCUGGU	UUCCCC GGC CAGAUGGC
5	1065 UCUCGGCC AGAA GGGCGG ACCAGAGAAAACACACGUUGGGUACAUUACCUGGU	CCGCCCA GAU GGCCGAGA
1116	GAGGCCUG AGAA GUGGUG ACCAGAGAAAACACACGUUGGGUACAUUACCUGGU	CACCAAC GUC CAGGCCUC
1198	AUTUGCUG AGAA GCCUGC ACCAGAGAAAACACACGUUGGGUACAUUACCUGGU	GCAGGCCA GCU CAGCAAU
1242	AGGUUGGA AGAA GCCUUA ACCAGAGAAAACACACGUUGGGUACAUUACCUGGU	UAAGGCCU GTU UCCAACCU
1253	GGCTUCUCA AGAA GGUUGG ACCAGAGAAAACACACGUUGGGUACAUUACCUGGU	CCAACCU GAC UGAGAGCC
10	1264 GGACUCGG AGAA GCUUC ACCAGAGAAAACACACGUUGGGUACAUUACCUGGU	GAGAGCC GCU CCGAGUCC
1291	GAUCAGGG AGAA GAGAGA ACCAGAGAAAACACACGUUGGGUACAUUACCUGGU	UCUTUCC GCU CCCUTGAUC
1298	CCGUGGGC AGAA GGGAGC ACCAGAGAAAACACACGUUGGGUACAUUACCUGGU	GUCCCU GAU CGCCACGG
1334	CCACCUUCG AGAA GAGACA ACCAGAGAAAACACACGUUGGGUACAUUACCUGGU	UGUUCUG GCU CGAGGGG
1353	UUCAUGAG AGAA GUGAAC ACCAGAGAAAACACACGUUGGGUACAUUACCUGGU	GUUCACCA GCC CUCAUGAA
15	1423 CAGCAGCA AGAA GCCAUC ACCAGAGAAAACACACGUUGGGUACAUUACCUGGU	GAUGGCCU GCC UGGUGUG
1427	UCUGCAGC AGAA GGCAGC ACCAGAGAAAACACACGUUGGGUACAUUACCUGGU	GCUGCCU GCU GCUGAGA
1430	CCAUCUGC AGAA GCAGGC ACCAGAGAAAACACACGUUGGGUACAUUACCUGGU	GCCUGCU GCU GCAGAUGG
1436	CGAAGUCC AGAA GCAGCA ACCAGAGAAAACACACGUUGGGUACAUUACCUGGU	UGCUGCA GAU GGACUTUCG
1447	CUUGGGAA AGAA GAAGUC ACCAGAGAAAACACACGUUGGGUACAUUACCUGGU	GACUUCG GCU UTUCCAAAG
20	1463 AAUCCACC AGAA GGUGCU ACCAGAGAAAACACACGUUGGGUACAUUACCUGGU	AGCACCU GCU GGUGGAAU

1521	GGGGAGAC AGAA GCGUGU ACCAGAGAAAACACAGUTUGGUUACAUUACCUGGU	ACACGGCU GAC GUCCUCGC
1530	CCCCGAUG AGAA GAGACC ACCAGAGAAAACACAGUTUGGUUACAUUACCUGGU	CGUCUCC GCC CAUCGGGG
1592	GUCUUCAG AGAA GAAGGA ACCAGAGAAAACACAGUTUGGUUACAUUACCUGGU	UCCTUUCU GUC CUGAAGAC
1690	CAGCUGGG AGAA GGAGCA ACCAGAGAAAACACAGUTUGGUUACAUUACCUGGU	UGCTUCCG GAU CCCAGCGU
5 1697	UAGCAGGC AGAA GGAUC ACCAGAGAAAACACAGUTUGGUUACAUUACCUGGU	GAUCCC A GCU GCCUGCUA
1700	CGUUAGCA AGAA CGUGGG ACCAGAGAAAACACAGUTUGGUUACAUUACCUGGU	CCCAGCU GCC UGCTUAAAG
1727	ACCAGCAC AGAA GCUCCC ACCAGAGAAAACACAGUTUGGUUACAUUACCUGGU	GGGAGCA GCC GUCCUGGU
1763	GGACCUCA AGAA GGGUCU ACCAGAGAAAACACAGUTUGGUUACAUUACCUGGU	AGACCCA GAC UGAGGUCC
1793	ACUCACTUG AGAA GGUUA ACCAGAGAAAACACAGUTUGGUUACAUUACCUGGU	UUAGCCU GCC CAGUGAGU
10 1825	CAGAGAGA AGAA GCCAGA ACCAGAGAAAACACAGUTUGGUUACAUUACCUGGU	UCUGGU GUC UCUCUCUG
1835	ACUTUGAGA AGAA GAGAGA ACCAGAGAAAACACAGUTUGGUUACAUUACCUGGU	UCUCUUCU GCC UCUCAAAGU

Claims

1. Nucleic acid molecule which blocks synthesis and/or expression of mRNAs associated with initial development, progression or regression of vascular disease.
- 5 2. The nucleic acid of claim 1 wherein said molecule is an enzymatic nucleic acid molecule.
3. The nucleic acid molecule of claim 2 wherein said nucleic acid molecule cleaves mRNA produced from the gene encoding CETP.
- 10 4. The nucleic acid molecule of claim 2, wherein the binding arms of said enzymatic nucleic acid molecule which contain sequences complementary to the sequences defined in any one of Tables II, IV, VI and VII.
- 15 5. The enzymatic nucleic acid molecule of claims 2 or 3 or 4, wherein said nucleic acid molecule is in a hammerhead motif.
- 20 6. The enzymatic nucleic acid molecule of claim 2 or 3 or 4, wherein said nucleic acid molecule is in a hairpin, hepatitis Delta virus, group I intron, VS nucleic acid or RNaseP nucleic acid motif.
7. The enzymatic nucleic acid molecule of any of claims 2 or 3 or 4, wherein said ribozyme comprises between 12 and 100 bases complementary to the RNA of said region.
- 25 8. The enzymatic nucleic acid of claim 7, wherein said ribozyme comprises between 14 and 24 bases complementary to the RNA of said region.

9. Enzymatic nucleic acid molecule consisting essentially of any sequence selected from the group of those shown in Tables III, V, VI and VII.

10. A mammalian cell including an enzymatic nucleic acid molecule of any of claims 1 or 2 or 3.

11. The cell of claim 10, wherein said cell is a human cell.

12. An expression vector comprising nucleic acid encoding the enzymatic nucleic acid molecule of any of claims 2 or 3 or 4, in a manner which allows expression and/or delivery of that enzymatic nucleic acid molecule within a mammalian cell.

13. A mammalian cell including an expression vector of claim 12.

15 14. The cell of claim 13, wherein said cell is a human cell.

15. A method for treatment of a patient having a condition associated with the level of CETP activity, wherein the said condition is selected from the group consisting of familial-hypercholesterolemia, atherosclerosis, peripheral vascular disease, dyslipidemia, hyperbetaalipoproteinemia, hypoalphalipoproteinemia, vascular complications of diabetes, transplant, atherectomy and angioplasty restenosis, wherein said patient is administered a therapeutically effective amount of an enzymatic nucleic acid molecule of claims 2 or 3 or 4.

16. A method for treatment of a condition related to the level of CETP activity by administering to a patient an expression vector of claim 12.

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17. The method of claims 15 or 16, wherein said patient is a human.

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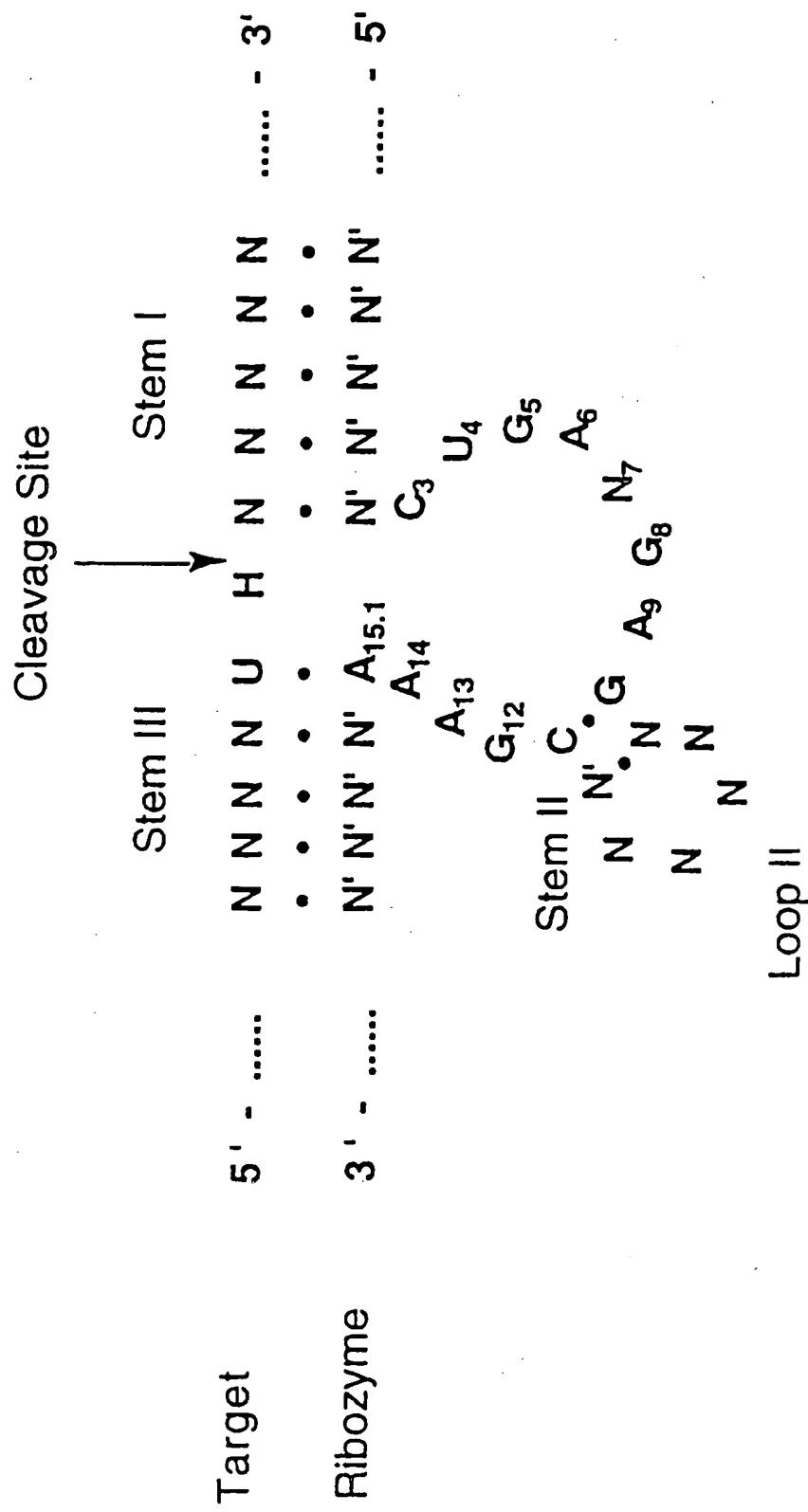
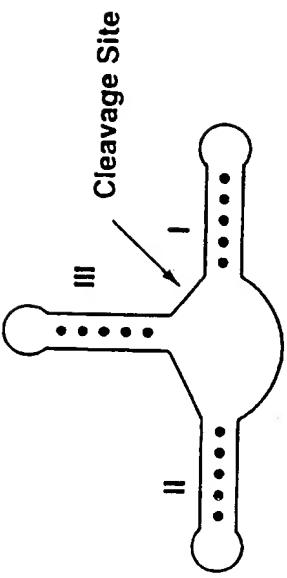


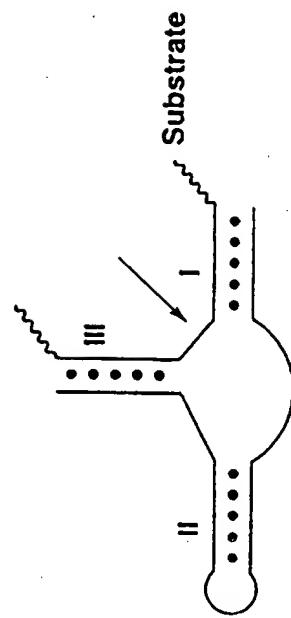
FIG. I.

FIG. 2b.



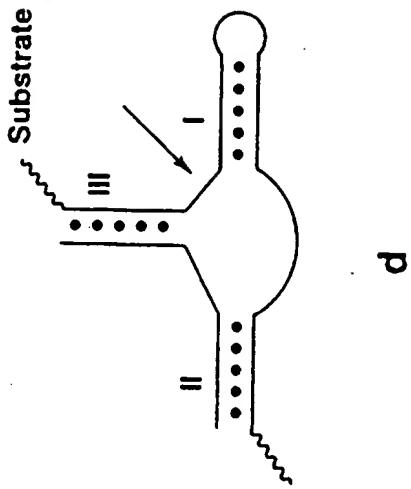
a

FIG. 2c.

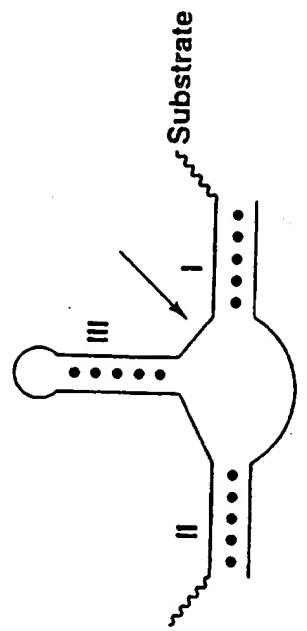


c

FIG. 2d.



d



b

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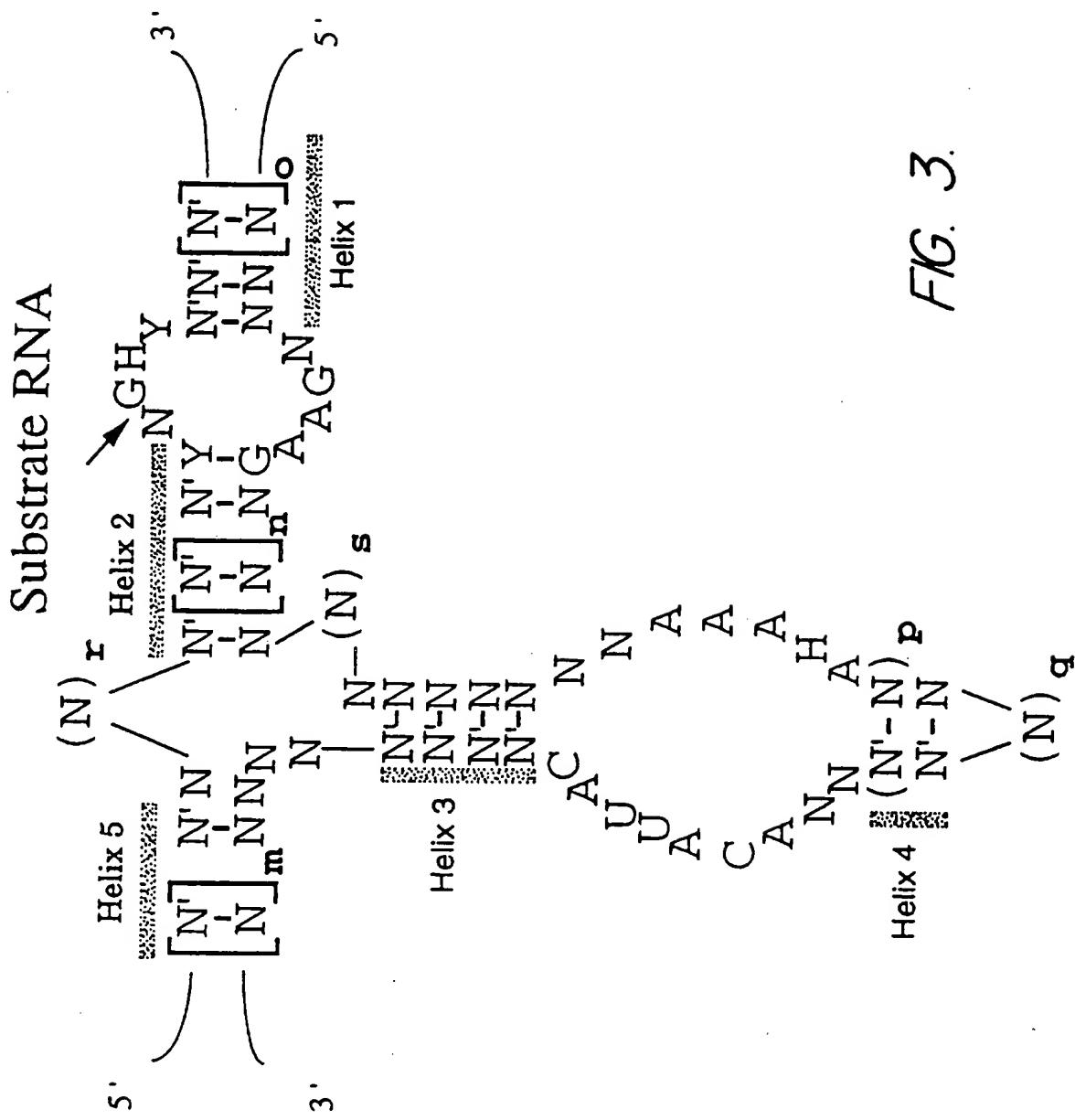


FIG. 3.

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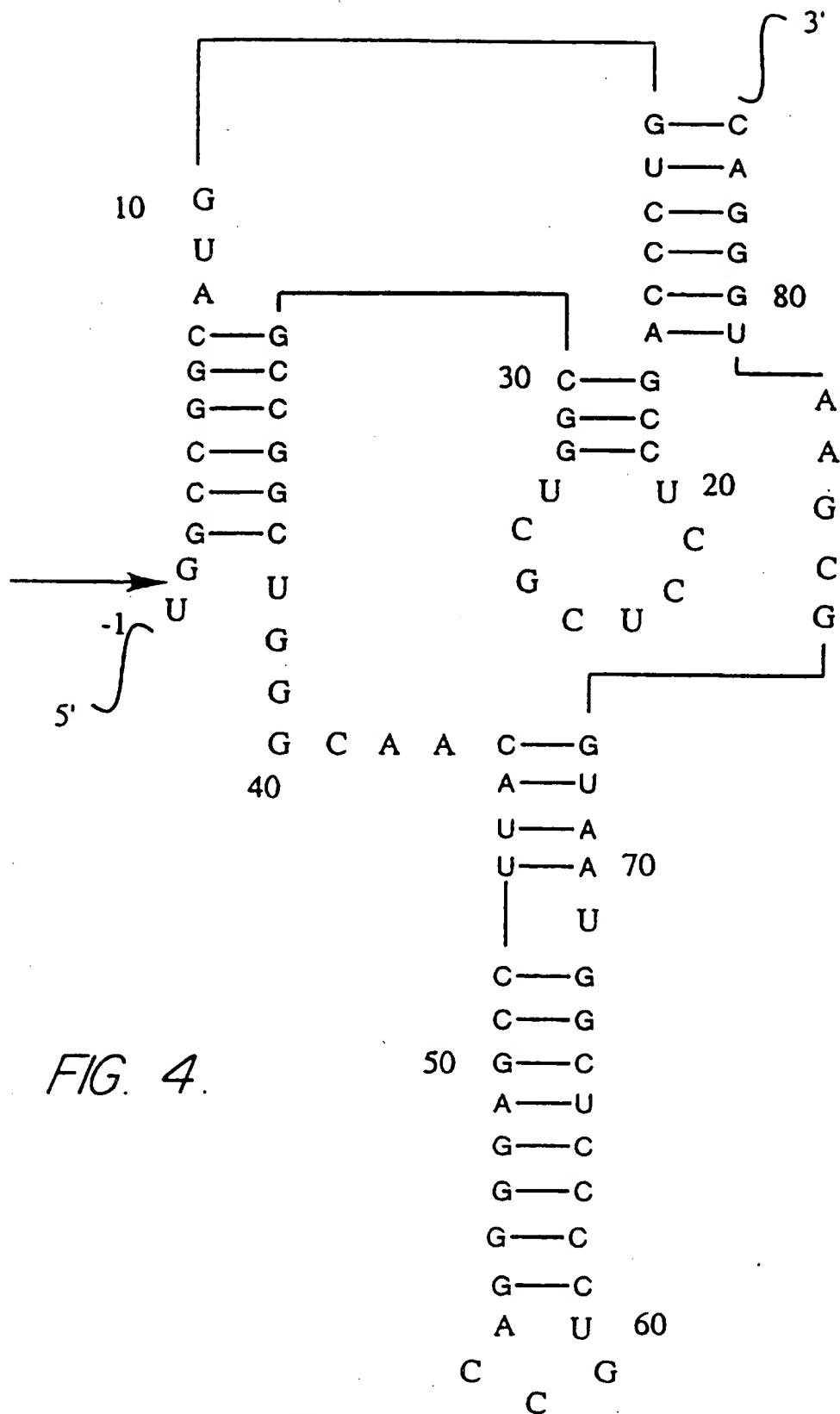


FIG. 5.

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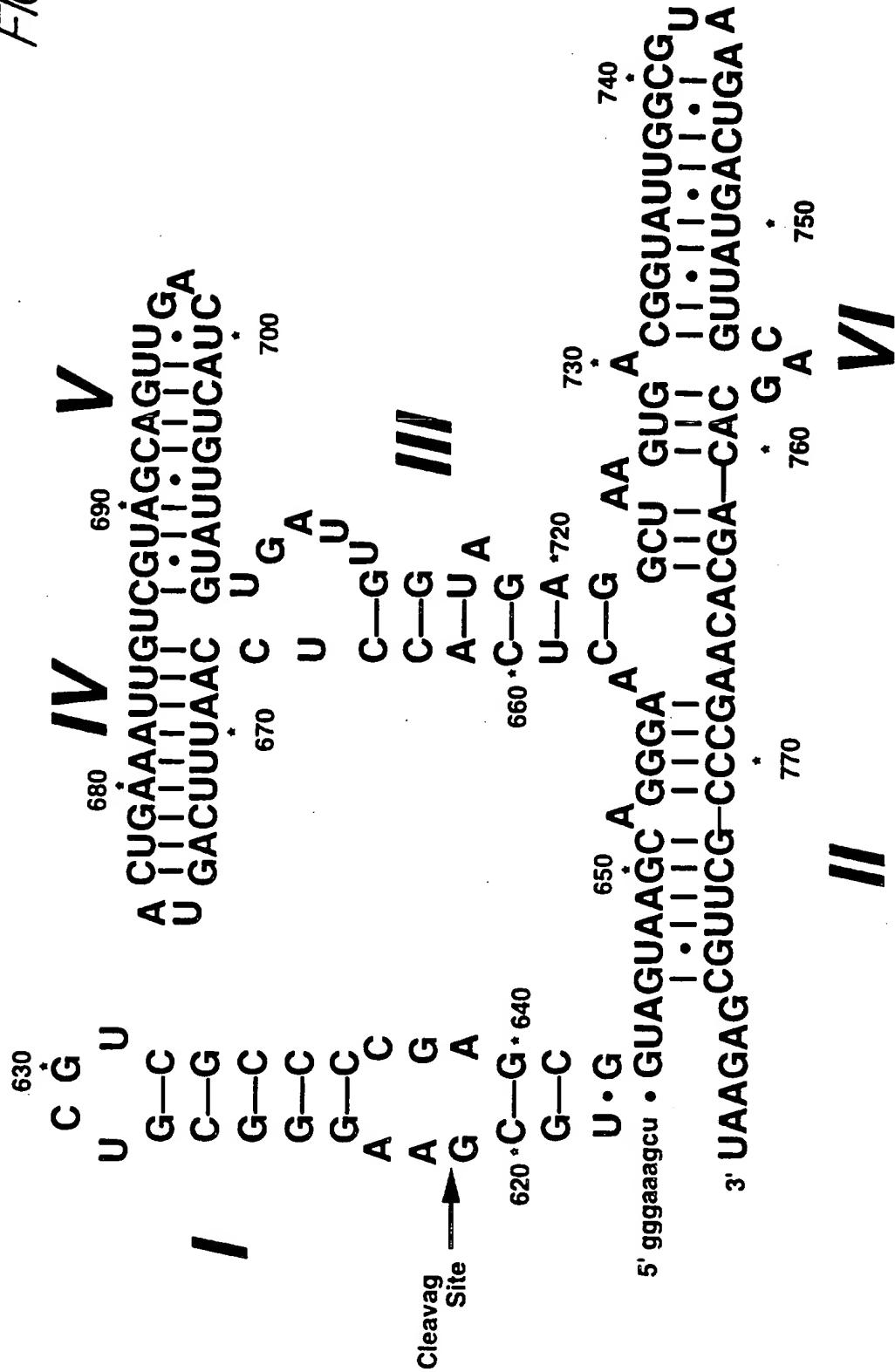
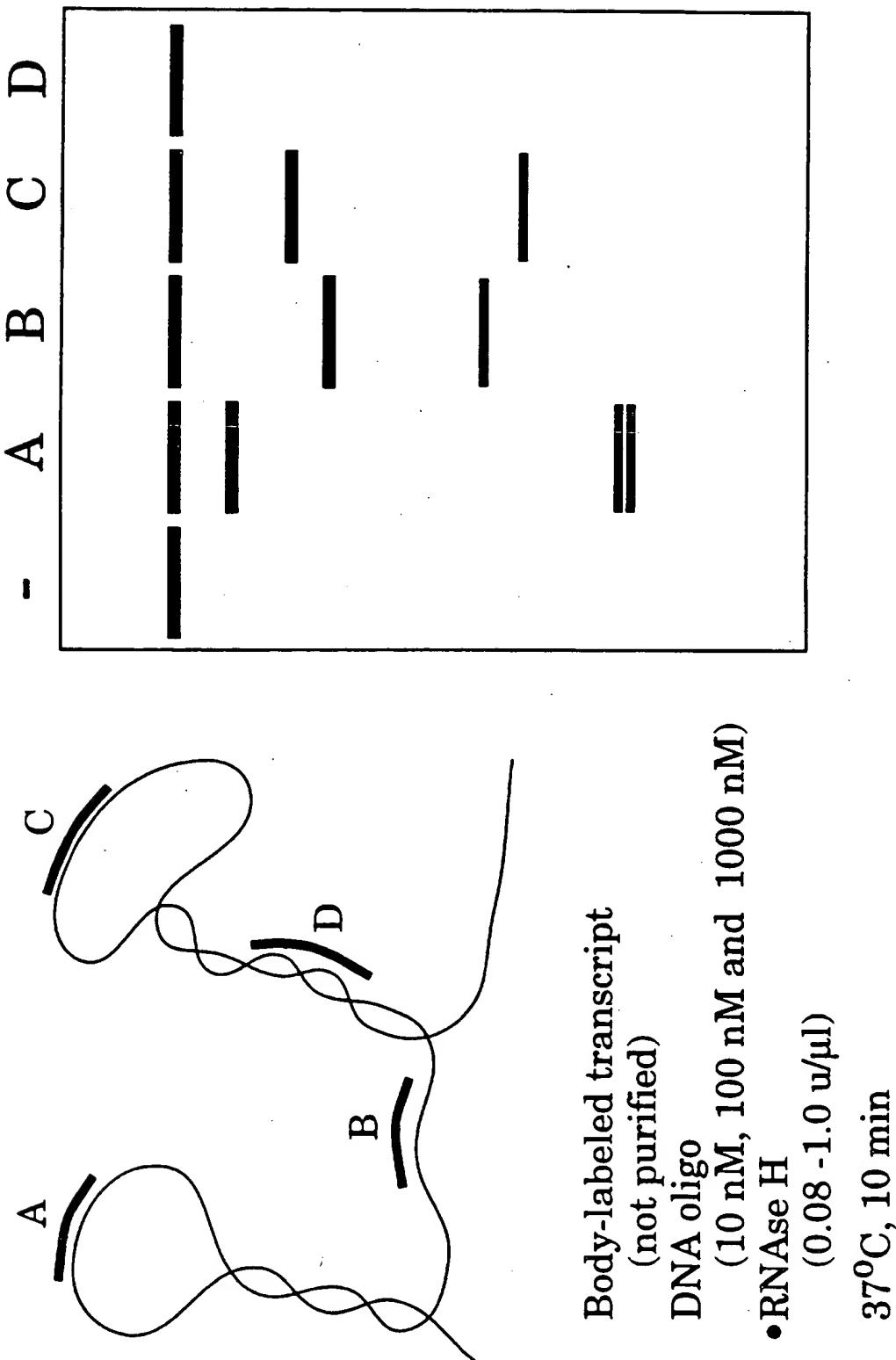


FIG. 6.



INTERNATIONAL SEARCH REPORT

Int'l Application No
PCT/US 95/16000

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 C12N15/52 C12N9/00 A61K31/70 C07H21/02 C12N5/10

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 C12N C07H A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO,A,94 02595 (RIBOZYME PHARMACEUTICALS INC) 3 February 1994 cited in the application see page 13, line 23 - line 35 see page 21, line 9 - page 25 see claims ---	1,2,5-8, 10-14
Y	LIPIDS, vol. 29, December 1994, pages 811-818, XP000568834 BISGAIER, C. ET AL.: "Cholesteryl ester transfer protein inhibition by PD 140195" cited in the application see the whole document ---	1-17
Y	-/-	1-17

Further documents are listed in the continuation of box C.

Patent family members are listed in annex.

* Special categories of cited documents :

- *'A' document defining the general state of the art which is not considered to be of particular relevance
- *'E' earlier document but published on or after the international filing date
- *'L' document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *'O' document referring to an oral disclosure, use, exhibition or other means
- *'P' document published prior to the international filing date but later than the priority date claimed

*'T' later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

*'X' document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

*'Y' document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

*'&' document member of the same patent family

Date of the actual completion of the international search

6 May 1996

Date of mailing of the international search report

10.05.96

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Authorized officer

Andres, S

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 95/16000

C(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	NATURE, vol. 327, 18 June 1987, LONDON GB, pages 632-634, XP002001819 DRAYNA, D. ET AL.: "Cloning and sequencing of human cholesteryl ester transfer protein cDNA" cited in the application ---	
P,X	JOURNAL OF BIOCHEMISTRY AND MOLECULAR BIOLOGY 28 (3). 243-248, 31 May 1995, XP000569967 LEE, M. ET AL.: "Inhibitory effects of antisense RNA on expression of cholesteryl ester transfer protein in vaccinia virus expression system." see the whole document -----	1

1

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 95/16000

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.: 15-17

because they relate to subject matter not required to be searched by this Authority, namely:

Remark: Although claims 15-17 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.

2. Claims Nos.:

because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. Claims Nos.:

because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a):

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 95/16000

Patent document cited in search report	Publication date	Patent family member(s)		Publication date
WO-A-9402595	03-02-94	AU-B-	4769893	14-02-94
		CA-A-	2140343	03-02-94
		EP-A-	0654077	24-05-95
		JP-T-	7509133	12-10-95